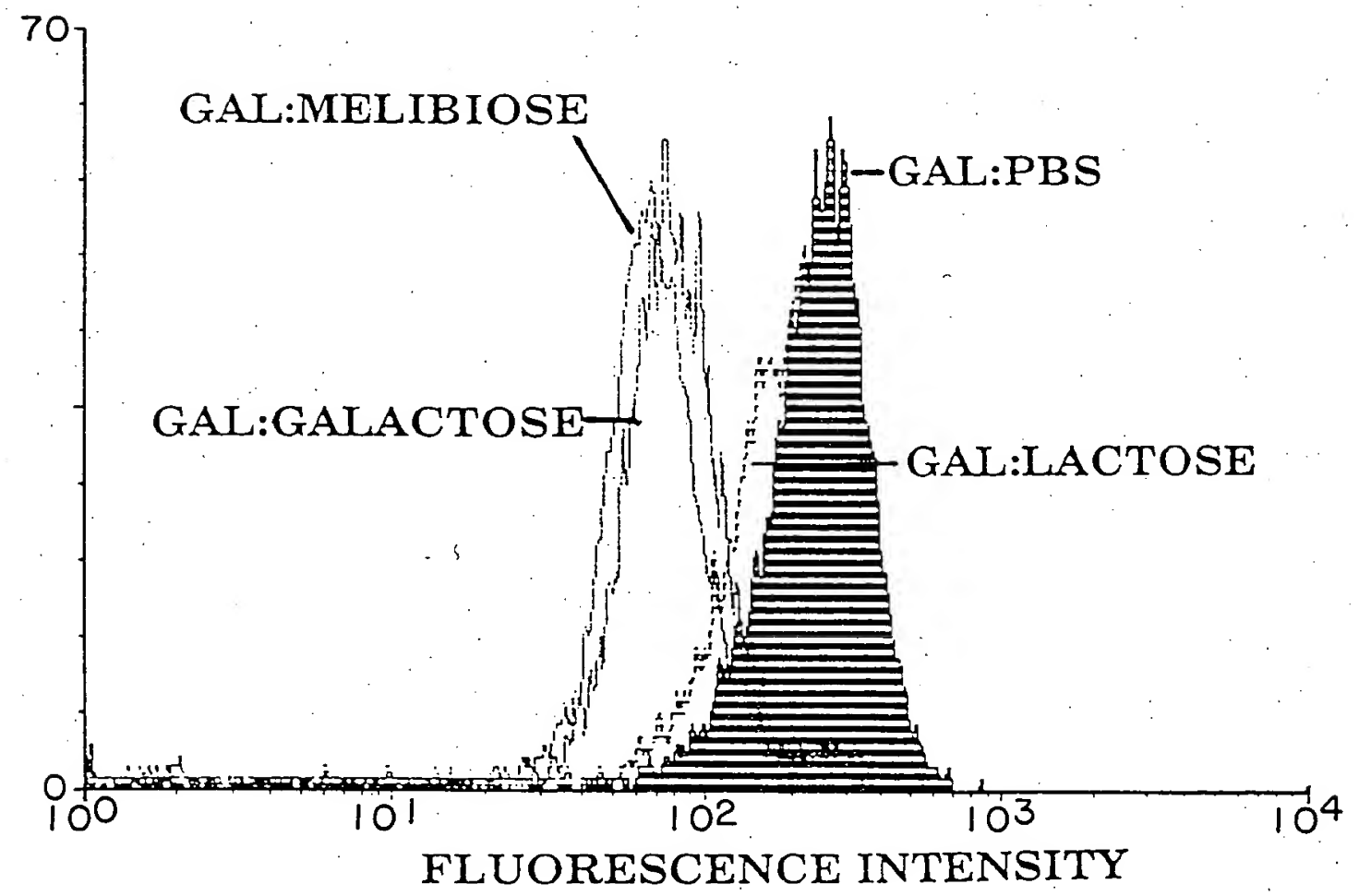


FIG. 1

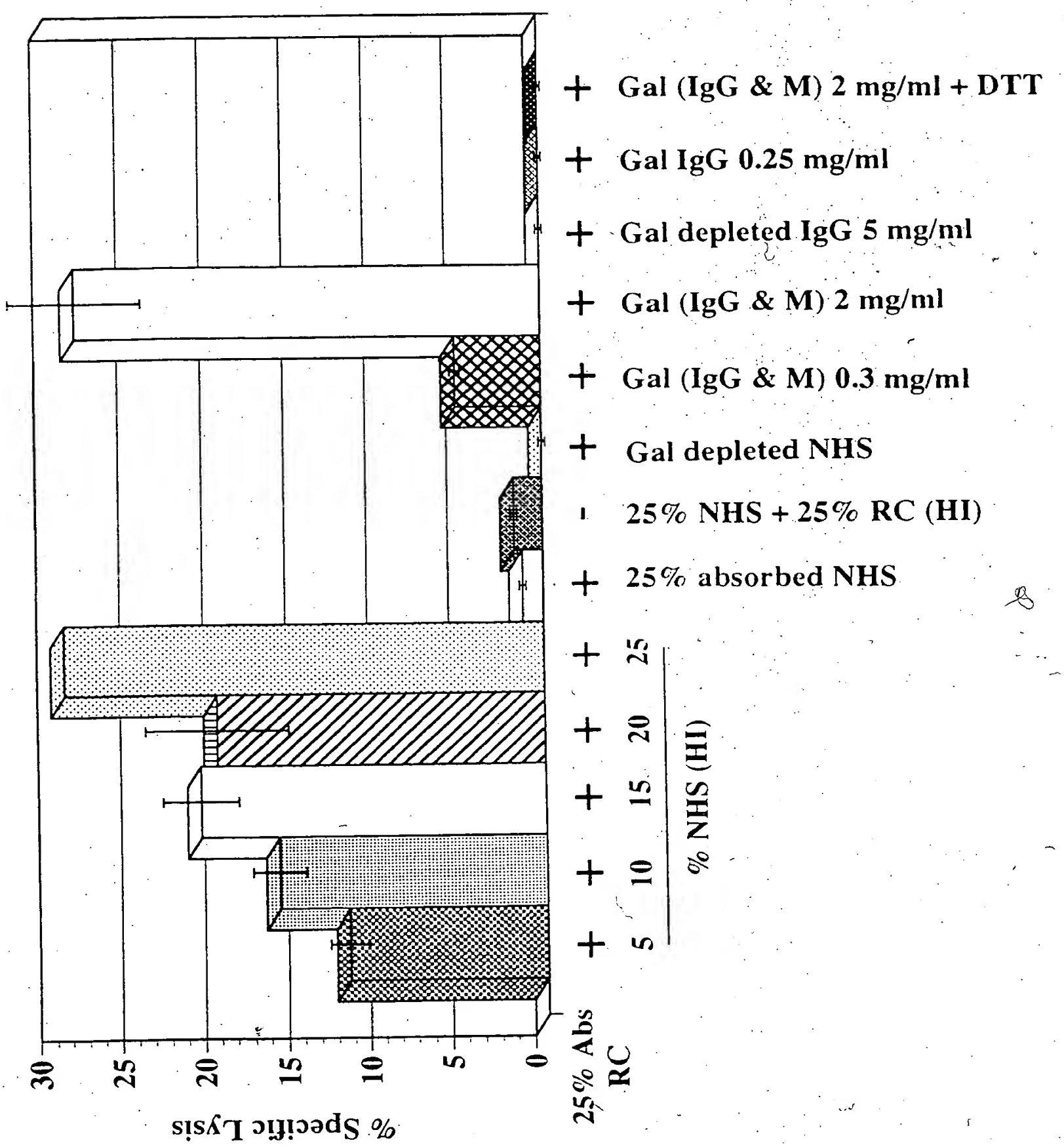


FIG. 2

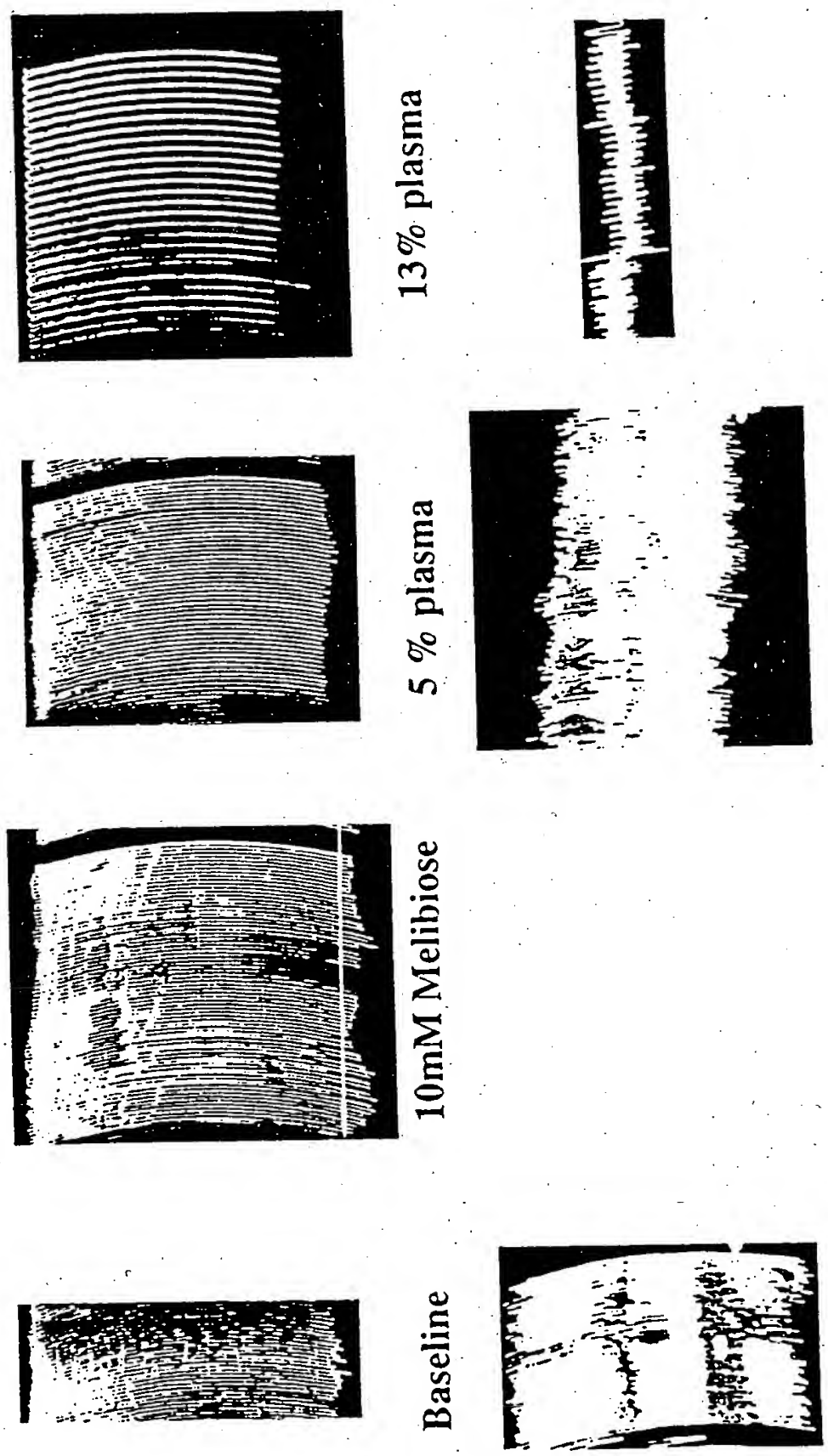


FIG. 3

```
PGTCD       1 ---------- ---------- ---------- ---------- ----------   50
BOVGSTA     1 CCGGGGGCCG GGCCGAGCTG GGAGCGTCGA GCCCGCTGCC CAGCGCCCGC   50
MUSGLYTNS   1 ---------- ---------- ---------- ---------- ----------   50

PGTCD      51 ---------- ---------- ---------- ---------- ----------  100
BOVGSTA    51 CGGCTCCCTC GCGCCCCTGC CCGCCGCCCC GGAGGAGCGC CCGGCGGCCG  100
MUSGLYTNS  51 ---------- ---------- ---------- ---------- ----------  100

PGTCD     101 ---------- ---------- ---------- ---------- ----------  150
BOVGSTA   101 GCCGACGGGA GCGCAGCGGC ACACCCCGCC CCGGCACGCC CGCGGGGCTC  150
MUSGLYTNS 101 ---------- ---------- ---------- ---------- ----------  150

PGTCD     151 ---------- ---------- ---------- ---------- ----------  200
BOVGSTA   151 GGGAGGAGGC AGCGCGCCGA CTGTTCCGGC AGCCGAGGAC GCCGCCGGGG  200
MUSGLYTNS 151 ---------- ---------- ---------- ---------- ----------  200

PGTCD     201 ---------- ---------- ---------- ---------- ----------  250
BOVGSTA   201 AGCCGAGGCG CCGGCCAGCC CCCAGCGCGC CCAGCTTCTG CGGATCAGGG  250
MUSGLYTNS 201 --------CG TCTTAGGAGG CTGGAGATTC TGGGTGGAGC CCTAGCCCTG  250

PGTCD     251 ---------- ---------- ---------- ---------- ----------  300
BOVGSTA   251 AAACCACGTG TCCTCAAGTG GCCAGCCAGC TGTCCCCAAG AGGAACTTGC  300
MUSGLYTNS 251 CCTTTTCTTA GCTGGCTGAC ACCTTCCCTT GTAGACTCTT CTTGGAATGA  300

                                                  Exon 1   Exon 2
PGTCD     301 ---------- ---------- ---------- ---------- ----------  350
BOVGSTA   301 CTGGCATTTG CACGGAAAGA CGAGACACTT CACAAAATCA ACGGAGTCAG  350
MUSGLYTNS 301 GAAGTACCGA TTCTGCTGAA GACCTCGCGC TCTCAGGCTC TGGGAGTTGG  350
```

FIG.4A

```
PGTCD       351 ---------- ---------- -------AGC CCTGCCTCCT TCTGCAGAGC  400
BOVGSTA     351 AAGGCTGCAC CTTCGCTTCC TCCC---AGC CCTGCCTCCT TCTGCAGAAC  400
MUSGLYTNS   351 AACCCTGTAC CTTCCTTTCC TCTGCTGAGC CCTGCCTCCT TCGGCAGGCC  400

PGTCD       401 AGAGCTCACT AGAACTT-GT TTC----GCC TTTTACTCTG GGGGGAGAGA  450
BOVGSTA     401 GGAGCTCAGT AGAACTT-GG TACTTTTGCC TTTTACTCTA GGAGGAGAGA  450
MUSGLYTNS   401 AGAGCTCGAC AGAAGCTCGG TTGCTTTGCT GTTTGCTTTG GAGGGAACAC  450

                          Exon 2 | Exon 3
PGTCD       451 AGCAGAGGAT GAG------- ---------- ---------- ----------  500
BOVGSTA     451 AGCAGACGAT GAG------- ---------- ---------- ----------  500
MUSGLYTNS   451 AGCTGACGAT GAGGCTGACT TTGAACTCAA GAGATCTGCT TACCCCAGTC  500

PGTCD       501 ---------- ---------- ---------- ---------- ----------  550
BOVGSTA     501 ---------- ---------- ---------- ---------- ----------  550
MUSGLYTNS   501 TCCTGGAATT AAAGGCCTGT ACTACCTTGC CTGGACCTAA GATTTTCATG  550

PGTCD       551 ---------- ---------- ---------- ---------- ----------  600
BOVGSTA     551 ---------- ---------- ---------- ---------- ----------  600
MUSGLYTNS   551 ATCACTATGC TTCAAGATCT CCATGTCAAC AAGATCTCCA TGTCAAGATC  600

                                                    Exon 3 | Exon 4
PGTCD       601 ---------- ---------- ---------- ---------- ---GAGAAAA  650
BOVGSTA     601 ---------- ---------- ---------- ---------- ---GAGAAAA  650
MUSGLYTNS   601 CAAGTCAGAA ACAAGTCTTC CATCCTCAAG ATCTGGATCA CAGGAGAAAA  650

PGTCD       651 TAATGAATGT CAAAGGAAGA GTGGTTCTGT CAATGCTGCT TGTCTCAACT  700
BOVGSTA     651 TAATGAATGT CAAAGGAAAA GTGATTCTGT CAATGCTGGT TGTCTCAACT  700
MUSGLYTNS   651 TAATGAATGT CAAGGGAAAA GTAATCCTGT TGATGCTGAT TGTCTCAACC  700
                Start
```

FIG. 4B

Exon 4 | Exon 5

```
PGTCD       701 GTAATGGTTG TGTTTTGGGA ATACATCAAC AGCCCAGAAG GTTCTTTGTT  750
BOVGSTA     701 GTCATTGTTG TGTTTTGGGA ATATATCCAC AGCCCAGAAG GCTCTTTGTT  750
MUSGLYTNS   701 GTGGTTGTCG TGTTTTGGGA ATATGTCAAC AGCCCAGACG GCTCTTTCTT  750
```

Exon 5 | Exon 6

```
PGTCD       751 CTGGATATAC CAGTCAAAAA ACCCAGAAGT TGGCAGCAGT GCTCAGAGGG  800
BOVGSTA     751 CTGGATAAAC CCATCAAGAA ACCCAGAAGT TGGTGGCAGC AGCATTCAGA  800
MUSGLYTNS   751 GTGGATATAT CACACAAAAA TTCCAGAGGT TGGTGAGAAC AGATGGCAGA  800
```

Exon 6 | Exon 7

```
PGTCD       801 GCTGGTGG-- -TTTCCGAGC TGGTTTAACA ATGGGACTCA CAGTTACCAC  850
BOVGSTA     801 AGGGCTGGTG GCTTCCGAGA TGGTTTAACA ATG------- --GTTACCAT  850
MUSGLYTNS   801 AGGACTGGTG GTTCCCAAGC TGGTTTAAAA ATGGGACCCA CAGTTATCAA  850

PGTCD       851 GAAGAAGAAG ACGCTATAGG CAACGAAAAG GAACAAAGAA AAGAAGACAA  900
BOVGSTA     851 GAAGAAGATG GAGACATAAA CGAAGAAAAG GAACAAAGAA ACGAAGACGA  900
MUSGLYTNS   851 GAAGACAACG TAGAAGGACG GAGAGAAAAG GGTAGAAATG GAGATCGCAT  900
```

Exon 7 | Exon 8

```
PGTCD       901 CAGAGGAGAG CTTCCGCTAG TGGACTGGTT TAATCCTGAG AAACGCCCAG  950
BOVGSTA     901 ---AAGCAAG CTTAAGCTAT CGGACTGGTT CAACCCATTT AAACGCCCCG  950
MUSGLYTNS   901 ---TGAAGAG CCTCAGCTAT GGGACTGGTT CAATCCAAAG AACCGCCCGG  950

PGTCD       951 AGGTCGTGAC CATAACCAGA TGGAAGGCTC CAGTGGTATG GGAAGGCACT 1000
BOVGSTA     951 AGGTTGTGAC CATGACGAAG TGGAAGGCTC CAGTGGTGTG GGAAGGCACT 1000
MUSGLYTNS   951 ATGTTTTGAC AGTGACCCCG TGGAAGGCGC CGATTGTGTG GGAAGGCACT 1000

PGTCD      1001 TACAACAGAG CCGTCTTAGA TAATTATTAT GCCAAACAGA AAATTACCGT 1050
BOVGSTA    1001 TACAACAGAG CCGTCTTAGA CAATTATTAT GCCAAGCAGA AAATTACCGT 1050
MUSGLYTNS  1001 TATGACACAG CTCTGCTGGA AAAGTACTAC GCCACACAGA AACTCACTGT 1050
```

FIG.4C

Exon 8 | Exon 9

```
PGTCD      1051 GGGCTTGACG GTTTTTGCTG TCGGAAGATA CATTGAGCAT TACTTGGAGG 1100
BOVGSTA    1051 CGGCCTGACG GTTTTCGCCG TCGGAAGATA CATTGAGCAT TACTTGGAGG 1100
MUSGLYTNS  1051 GGGGCTGACA GTGTTTGCTG TGGGAAAGTA CATTGAGCAT TACTTAGAAG 1100

PGTCD      1101 AGTTCTTAAT ATCTGCAAAT ACATACTTCA TGGTTGGCCA CAAAGTCATC 1150
BOVGSTA    1101 AGTTCTTAAC GTCTGCTAAT AAGCACTTCA TGGTGGGCCA CCCAGTCATC 1150
MUSGLYTNS  1101 ACTTTCTGGA GTCTGCTGAC ATGTACTTCA TGGTTGGCCA TCGGGTCATA 1150

PGTCD      1151 TTTTACATCA TGGTGGATGA TATCTCCAGG ATGCCTTTGA TAGAGCTGGG 1200
BOVGSTA    1151 TTTTATATCA TGGTAGATGA TGTCTCCAGG ATGCCTTTGA TAGAGTTGGG 1200
MUSGLYTNS  1151 TTTTACGTCA TGATAGATGA CACCTCCCGG ATGCCTGTCG TGCACCTGAA 1200

PGTCD      1201 TCCTCTGCGT TCCTTTAAAG TGTTTGAGAT CAAGTCCGAG AAGAGGTGGC 1250
BOVGSTA    1201 TCCTCTGCGC TCCTTCAAAG TGTTTAAGAT CAAGCCTGAG AAGAGGTGGC 1250
MUSGLYTNS  1201 CCCTCTACAT TCCTTACAAG TCTTTGAGAT CAGGTCTGAG AAGAGGTGGC 1250

PGTCD      1251 AAGACATCAG CATGATGCGC ATGAAGACCA TCGGGGAGCA CATCCTGGCC 1300
BOVGSTA    1251 AGGACATCAG CATGATGCGC ATGAAGACTA TCGGGGAGCA CATTGTGGCC 1300
MUSGLYTNS  1251 AGGATATCAG CATGATGCGC ATGAAGACCA TTGGGGAGCA CATCCTGGCC 1300

PGTCD      1301 CACATCCAGC ACGAGGTGGA CTTCCTCTTC TGCATGGACG TGGATCAGGT 1350
BOVGSTA    1301 CACATCCAGC ATGAGGTTGA CTTCCTTTTC TGCATGGATG TGGACCAGGT 1350
MUSGLYTNS  1301 CACATCCAGC ACGAGGTCGA CTTCCTCTTC TGCATGGACG TGGATCAAGT 1350

PGTCD      1351 CTTCCAAAAC AACTTTGGGG TGGAGACCCT GGGCCAGTCG GTGGCTCAGC 1400
BOVGSTA    1351 CTTCCAAGAC AAGTTTGGGG TGGAGACCCT GGGCGAGTCG GTGGCCCAGC 1400
MUSGLYTNS  1351 CTTTCAAGAC AACTTCGGGG TGGAAACTCT GGGCCAGCTG GTAGCACAGC 1400
```

FIG. 4D

```
PGTCD      1401 TACAGGCCTG GTGGTACAAG GCACATCCTG ACGAGTTCAC CTACGAGAGG 1450
BOVGSTA    1401 TACAAGCCTG GTGGTACAAG GCAGATCCCA ATGACTTCAC CTACGAGAGG 1450
MUSGLYTNS  1401 TCCAGGCCTG GTGGTACAAG GCCAGTCCCG AGAAGTTCAC CTATGAGAGG 1450

PGTCD      1451 CGGAAGGAGT CCGCAGCCTA CATTCCGTTT GGCCAGGGGG ATTTTTATTA 1500
BOVGSTA    1451 CGGAAGGAGT CTGCAGCATA CATTCCCTTC GGCGAAGGGG ATTTTTATTA 1500
MUSGLYTNS  1451 CGGGAACTGT CGGCCGCGTA CATTCCATTC GGAGAGGGGG ATTTTTACTA 1500

PGTCD      1501 CCACGCAGCC ATTTTTGGGG GAACACCCAC TCAGGTTCTA AACATCACTC 1550
BOVGSTA    1501 CCATGCAGCC ATTTTTGGGG GAACACCCAC TCAGGTCCTT AACATCACCC 1550
MUSGLYTNS  1501 CCACGCGGCC ATTTTTGGAG GAACGCCTAC TCACATTCTC AACCTCACCA 1550

PGTCD      1551 AGGAGTGCTT CAAGGGAATC CTCCAGGACA AGGAAAATGA CATAGAAGCC 1600
BOVGSTA    1551 AGGAATGCTT CAAAGGAATC CTCAAGGACA AGAAAAATGA CATAGAAGCC 1600
MUSGLYTNS  1551 GGGAGTGCTT TAAGGGGATC CTCCAGGACA AGAAACATGA CATAGAAGCC 1600

PGTCD      1601 GAGTGGCATG ATGAAAGCCA TCTAAACAAG TATTTCCTTC TCAACAAACC 1650
BOVGSTA    1601 CAATGGCATG ATGAAAGCCA TCTAAACAAG TATTTCCTTC TCAACAAACC 1650
MUSGLYTNS  1601 CAGTGGCATG ATGAGAGCCA CCTCAACAAA TACTTCCTTT TCAACAAACC 1650

PGTCD      1651 CACTAAAATC TTATCCCCAG AATACTGCTG GGATTATCAT ATAGGCATGT 1700
BOVGSTA    1651 TACTAAAATC TTATCCCCGG AATACTGCTG GGATTATCAC ATAGGCCTAC 1700
MUSGLYTNS  1651 CACTAAAATC CTATCTCCAG AGTATTGCTG GGACTATCAG ATAGGCCTGC 1700

PGTCD      1701 CTGTGGATAT TAGGATTGTC AAGATAGCTT GGCAGAAAAA AGAGTATAAT 1750
BOVGSTA    1701 CTGCGGATAT TAAGCTTGTC AAGATGTCTT GGCAGACAAA AGAGTATAAT 1750
MUSGLYTNS  1701 CTTCAGATAT TAAAAGTGTC AAGGTAGCTT GGCAGACAAA AGAGTATAAT 1750
```

FIG.4E

```
PGTCD      1751 TTGGTTAGAA ATAACATCTG ACTTTAAATT GTGCCAGCAG TTTTCTGAAT 1800
BOVGSTA    1751 GTGGTTAGAA ATAATGTCTG ACTT-----T GTGCCAGTAC ATTTCTGAAT 1800
MUSGLYTNS  1751 TTGGTTAGAA ATAATGTCTG ACTTCAAATT GTG------- --ATGGAAAC 1800
                                    Stop

PGTCD      1801 TTGAAAGAGT ATTACTCTGG CTACTTCCTC AGAGAAGTAG ---CACTTAA 1850
BOVGSTA    1801 TTGAGAGAGT ATTATTCTGG CTACTTCCTC AGAAAAGTAA ---CACTTAA 1850
MUSGLYTNS  1801 TTGACAC--T ATTACTCTGG CTAATTCCTC AAACAAGTAG CAACACTTGA 1850

PGTCD      1851 TTTTAACTTT TAAAAAAATA CTAACAAAA- ----TACCAA CACAGTAA-G 1900
BOVGSTA    1851 TTTTAACTTA AAAAAAAATA CTAACAAAA- ----GACCAA CACAGCAA-A 1900
MUSGLYTNS  1851 TTTCAACTTT TAAAAGAA-A CAATCAAAAC CAAAACCCAC TACCATGGCA 1900

PGTCD      1901 TACATATTAT TCTTCCTTGC AACTTTGAGC CTTGTCAAAT GGGAGAATGA 1950
BOVGSTA    1901 TACATATTAT TTCTCCTTGT AACTTTGAGC CTTGTAATAC GGGAGAATGA 1950
MUSGLYTNS  1901 AACAGATGAT TTCTCCT-GA CACCTTGAGC CT-GTAATAT GTGAGAAAGA 1950

PGTCD      1951 CTCTGTGG-- --TAATCAGA TGTAAATTCC CAGTGATTTC .......... 2000
BOVGSTA    1951 ACCTGTGG-- --TAATCAGA TGTAAATTCC CAGTGATTTC TTACCTATTT 2000
MUSGLYTNS  1951 GTCTATGGCA AGTAATCAGG TATAAATTCT CAATGATTTC TTATATATTC 2000

PGTCD      2001 .......... .......... .......... .......... .......... 2050
BOVGSTA    2001 TTGGTTGTGG GGGCGGGGAA TGGATACACC ATCAGTTGAA CC......... 2050
MUSGLYTNS  2001 TGGGTCTTGG GAAAACTTGA TTCTAGAAAT CAAAATTAAT TTGACAAAGG 2050

PGTCD      2051 .......... .......... .......... .......... .......... 2100
BOVGSTA    2051 .......... .......... .......... .......... .......... 2100
MUSGLYTNS  2051 AAAAGCAGAT GCCGGAAACT TCTTCCCAGT CTGTCATACA ATTCACCACT 2100
```

FIG. 4F

```
PGTCD      2101 .......... .......... .......... .......... .......... 2150
BOVGSTA    2101 .......... .......... .......... .......... .......... 2150
MUSGLYTNS  2101 GGCCAGGTGC TGAGAGAAGC ATTAGGGAAC AGTGTGGGTT GTGTCAGAGT 2150

PGTCD      2151 .......... .......... .......... .......... .......... 2200
BOVGSTA    2151 .......... .......... .......... .......... .......... 2200
MUSGLYTNS  2151 TGGACGGCTC CATCCCTTTG GCTTCATTAT CTTCCTCCTC ATGGAGATTC 2200

PGTCD      2201 .......... .......... .......... .......... .......... 2250
BOVGSTA    2201 .......... .......... .......... .......... .......... 2250
MUSGLYTNS  2201 TAAAGCAACC CAGAGAGGCT TTGCAGCCAG AGACCTTTAA TAAGGATGCC 2250

PGTCD      2251 .......... .......... .......... .......... .......... 2300
BOVGSTA    2251 .......... .......... .......... .......... .......... 2300
MUSGLYTNS  2251 AATGTGACCA TCAGTCTGTA AAAGCTGATG GCTCCAGGAG CGCTGGCAGT 2300

PGTCD      2301 .......... .......... .......... .......... .......... 2350
BOVGSTA    2301 .......... .......... .......... .......... .......... 2350
MUSGLYTNS  2301 CCAGGCCCCA CTAGGCTATT GTTTCTGTCC TGGGCATAAA GGAGGCAGAG 2350

PGTCD      2351 .......... .......... .......... .......... .......... 2400
BOVGSTA    2351 .......... .......... .......... .......... .......... 2400
MUSGLYTNS  2351 AGTGCCAATA GGTACTTTGG TGGCACATGT TCAGAGTCCA GGAAAAATCA 2400

PGTCD      2401 .......... .......... .......... .......... .......... 2450
BOVGSTA    2401 .......... .......... .......... .......... .......... 2450
MUSGLYTNS  2401 AGGGTGACCA CTTAGAGGGA CATAGGACTT GGGGTTGGTG ATTGAACTGA 2450
```

FIG. 4G

```
PGTCD      2451 .......... .......... .......... .......... .......... 2500
BOVGSTA    2451 .......... .......... .......... .......... .......... 2500
MUSGLYTNS  2451 GTTACAAACA CAGACAGCTT TCTTCAGGAT GACTAACAGC AGGAATTGAA 2500

PGTCD      2501 .......... .......... .......... .......... .......... 2550
BOVGSTA    2501 .......... .......... .......... .......... .......... 2550
MUSGLYTNS  2501 TGGAAAGTGT GTTCATTTTG TTTTGCCCAA ATTGTATTCA TGCTGTTAGC 2550

PGTCD      2551 .......... .......... .......... .......... .......... 2600
BOVGSTA    2551 .......... .......... .......... .......... .......... 2600
MUSGLYTNS  2551 TTTGTGTGTT GAGCCCTGTG GAGAGGGTGT GACTGTATCA GGGAAGGAGA 2600

PGTCD      2601 .......... .......... .......... .......... .......... 2650
BOVGSTA    2601 .......... .......... .......... .......... .......... 2650
MUSGLYTNS  2601 GTACCTCAGC GGACTGAGGA CCAGCACCCT ATTATATCAG AAGACAATCT 2650

PGTCD      2651 .......... .......... .......... .......... .......... 2700
BOVGSTA    2651 .......... .......... .......... .......... .......... 2700
MUSGLYTNS  2651 CTCATCATCA GGTCCTACCT ACAACCTGCT CTGAACCTCC GAGTTCCTCA 2700

PGTCD      2701 .......... .......... .......... .......... .......... 2750
BOVGSTA    2701 .......... .......... .......... .......... .......... 2750
MUSGLYTNS  2701 GCCCATCGTG TTCCAGTGTG GGGGCCTGTA TGGAGCAGGT GACTGAAGAC 2750

PGTCD      2751 .......... .......... .......... .......... .......... 2800
BOVGSTA    2751 .......... .......... .......... .......... .......... 2800
MUSGLYTNS  2751 AAAGCCCCCT GTCACATGAC CTCATTTCCC CTGCTCTAGT ACTATGCAAG 2800
```

FIG. 4H

```
PGTCD      2801 .......... .......... .......... .......... .......... 2850
BOVGSTA    2801 .......... .......... .......... .......... .......... 2850
MUSGLYTNS  2801 TGTGACAGCC AGCCAGCCAG ATGTACTGGA CAACATAGGA ACCGACTTTA 2850

PGTCD      2851 .......... .......... .......... .......... .......... 2900
BOVGSTA    2851 .......... .......... .......... .......... .......... 2900
MUSGLYTNS  2851 TGGCAATGGG AGCCGCAGTC ACTACAACGG AGCTGCTGAA GGTTCTGTTC 2900

PGTCD      2901 .......... .......... .......... .......... .......... 2950
BOVGSTA    2901 .......... .......... .......... .......... .......... 2950
MUSGLYTNS  2901 CCCGCTCTGA GAGCCTGCAG GAGCCCCTGT ATAGGTGGTT CTCAACCTAT 2950

PGTCD      2951 .......... .......... .......... .......... .......... 3000
BOVGSTA    2951 .......... .......... .......... .......... .......... 3000
MUSGLYTNS  2951 GGGTCGCGAC CCCTTTGGGA AGTGTTAAAT GACCCTTTCA CAGGTGTCCC 3000

PGTCD      3001 .......... .......... .......... .......... .......... 3050
BOVGSTA    3001 .......... .......... .......... .......... .......... 3050
MUSGLYTNS  3001 CTAAGACGGT TAAAAAACAT AGATATTTCC ACTCTGACTG GTAACAGTAG 3050

PGTCD      3051 .......... .......... .......... .......... .......... 3100
BOVGSTA    3051 .......... .......... .......... .......... .......... 3100
MUSGLYTNS  3051 CAGAATTACA GTTATGAAAT AGCAAGGGAA ATAATTCTGG GGTTCGTGTC 3100
```

FIG. 41

```
                                                Ex4 ▼ Ex5      Ex5 ▼ Ex6
PGT[Frame 1]   1 MNVKGRVVLS MLLVSTVMVV FWEYINSPEG SLFWIYQSKN PEVG-SSAQR  50
BGT[Frame 1]   1 MNVKGKVILS MLVVSTVIVV FWEYIHSPEG SLFWINPSRN PEVGGSSIQK  50
MGT[Frame 1]   1 MNVKGKVILL MLIVSTVVVV FWEYVNSPDG SFLWIYHTKI PEVGENRWQK  50

                                  Ex6 ▼ Ex7                        Ex7 ▼ Ex8
PGT[Frame 1]  51 GWWFPSWFNN GTHSYHEEED AIGNEKEQRK EDNRGELPLV DWFNPEKRPE 100
BGT[Frame 1]  51 GWWLPRWFNN G---YHEEDG DINEEKEQRN ED-ESKLKLS DWFNPFKRPE 100
MGT[Frame 1]  51 DWWFPSWFKN GTHSYQEDNV EGRREK-GRN GDRIEEPQLW DWFNPKNRPD 100

                                                Ex8 ▼ Ex9
PGT[Frame 1]101 VVTITRWKAP VVWEGTYNRA VLDNYNAKQK ITVGLTVFAV GRYIEHYLEE 150
BGT[Frame 1]101 VVTMTKWKAP VVWEGTYNRA VLDNYYAKQK ITVGLTVFAV GRYIEHYLEE 150
MGT[Frame 1]101 VLTVTPWKAP IVWEGTYDTA LLEKYYATQK LTVGLTVFAV GKYIEHYLED 150

PGT[Frame 1]151 FLISANTYFM VGHKVIFYIM VDDISRMPLI ELGPLRSFKV FEIKSEKRWQ 200
BGT[Frame 1]151 FLTSANKHFM VGHPVIFYIM VDDVSRMPLI ELGPLRSFKV FKIKPEKRWQ 200
MGT[Frame 1]151 FLESADMYFM VGHRVIFYVM IDDTSRMPVV HLNPLHSLQV FEIRSEKRWQ 200
```

FIG. 5A

```
PGT[Frame 1]201 DISMMRMKTI GEHILAHIQH EVDFLFCMDV DQVFQNNFGV ETLGQSVAQL 250
BGT[Frame 1]201 DISMMRMKTI GEHIVAHIQH EVDFLFCMDV DQVFQDKFGV ETLGESVAQL 250
MGT[Frame 1]201 DISMMRMKTI GEHILAHIQH EVDFLFCMDV DQVFQDNFGV ETLGQLVAQL 250

PGT[Frame 1]251 QAWWYKAHPD EFTYERRKES AAYIPFGQGD FYYHAAIFGG TPTQVLNITQ 300
BGT[Frame 1]251 QAWWYKADPN DFTYERRKES AAYIPFGEGD FYYHAAIFGG TPTQVLNITQ 300
MGT[Frame 1]251 QAWWYKASPE KFTYERRELS AAYIPFGEGD FYYHAAIFGG TPTHILNLTR 300

PGT[Frame 1]301 ECFKGILQDK ENDIEAEWHD ESHLNKYFLL NKPTKILSPE YCWDYHIGMS 350
BGT[Frame 1]301 ECFKGILKDK KNDIEAQWHD ESHLNKYFLL NKPTKILSPE YCWDYHIGLP 350
MGT[Frame 1]301 ECFKGILQDK KHDIEAQWHD ESHLNKYFLF NKPTKILSPE YCWDYQIGLP 350

PGT[Frame 1]351 VDIKIVKIAW QKKEYNLVRN NI*..... ..... ..... 400
BGT[Frame 1]351 ADIKLVKMSW QTKEYNVVRN NV*..... ..... ..... 400
MGT[Frame 1]351 SDIKSVKVAW QTKEYNLVRN NV*..... ..... ..... 400
```

FIG.5B

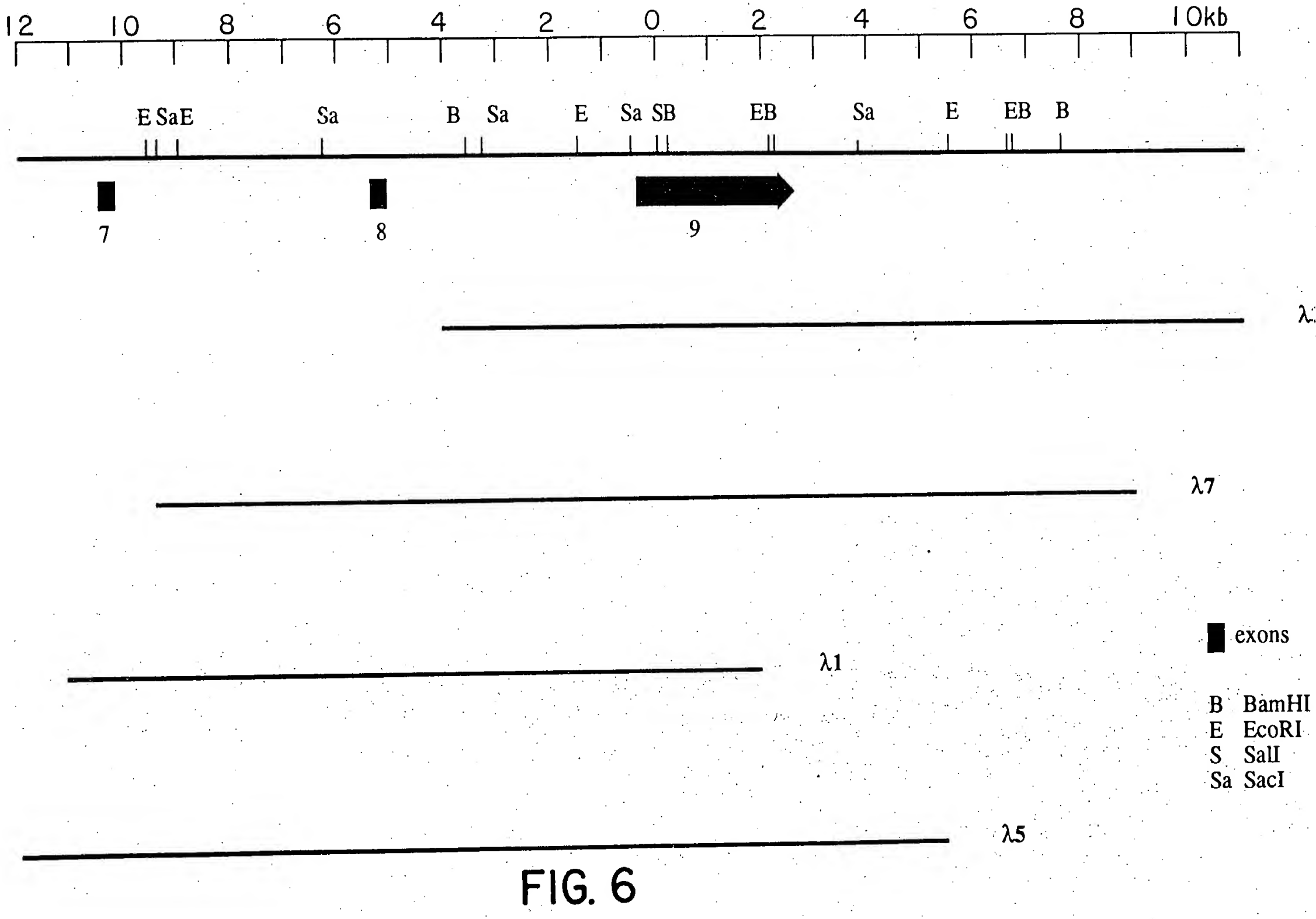
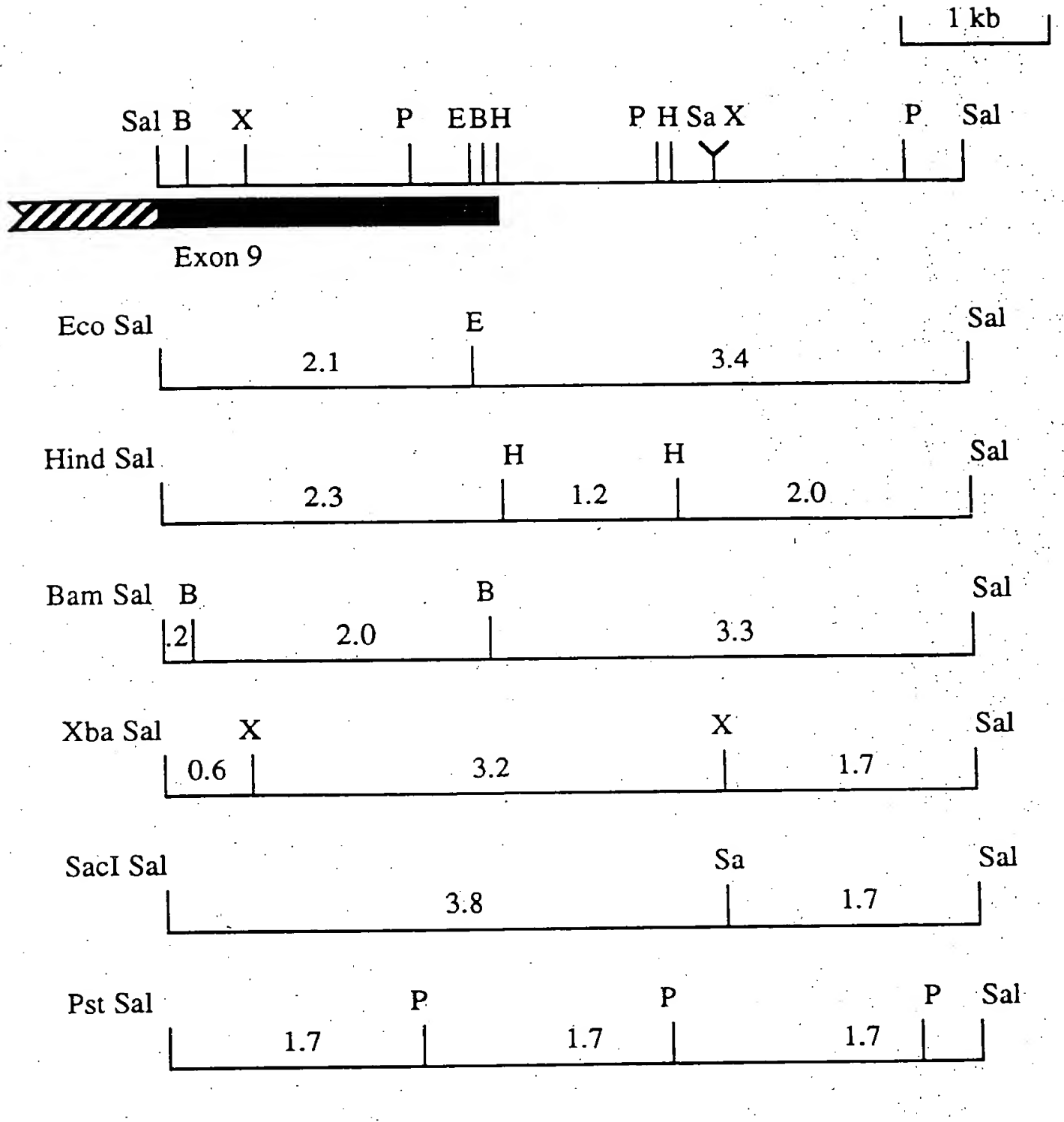


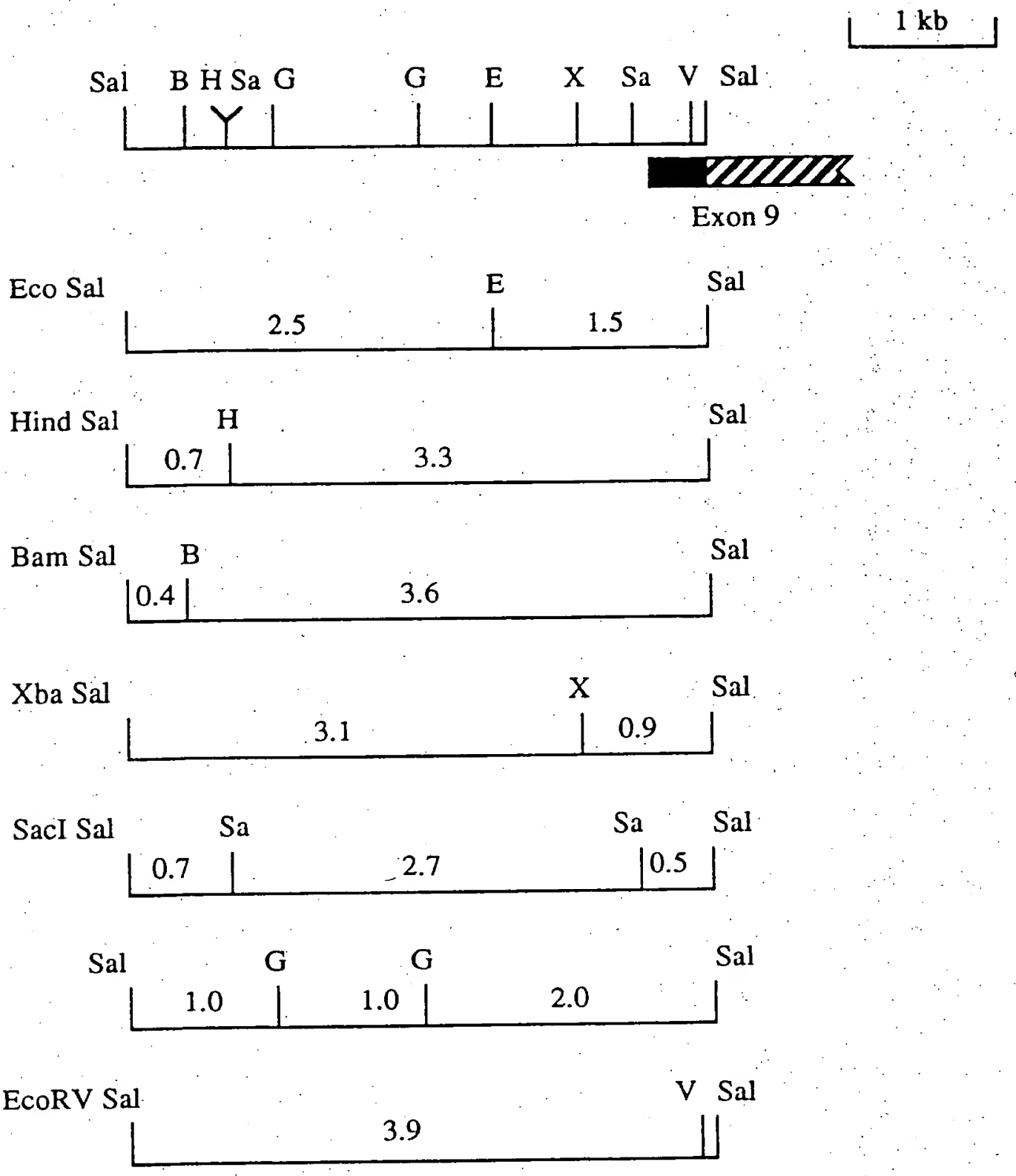
FIG. 6



No sites for: BglII, Nde, PvuI, Xho, Kpn, SacII, EcoRV, Sma, Cla, Apa, Not

pBS+KS: .... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn ....

FIG. 7



A	ApaI
B	BamHI
C	ClaI
E	EcoRI
G	BglII
H	HindIII
K	KpnI
N	NotI
P	PstI
S	Sal
Sa	SacI
V	EcoRV
X	XbaI
Xh	XhoI

No sites for: Nde, PvuI, Xho, Kpn, SacII, Sma, Cla, Apa, Not

Unmapped sites for: Pst, PvuII

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn ....

FIG. 8

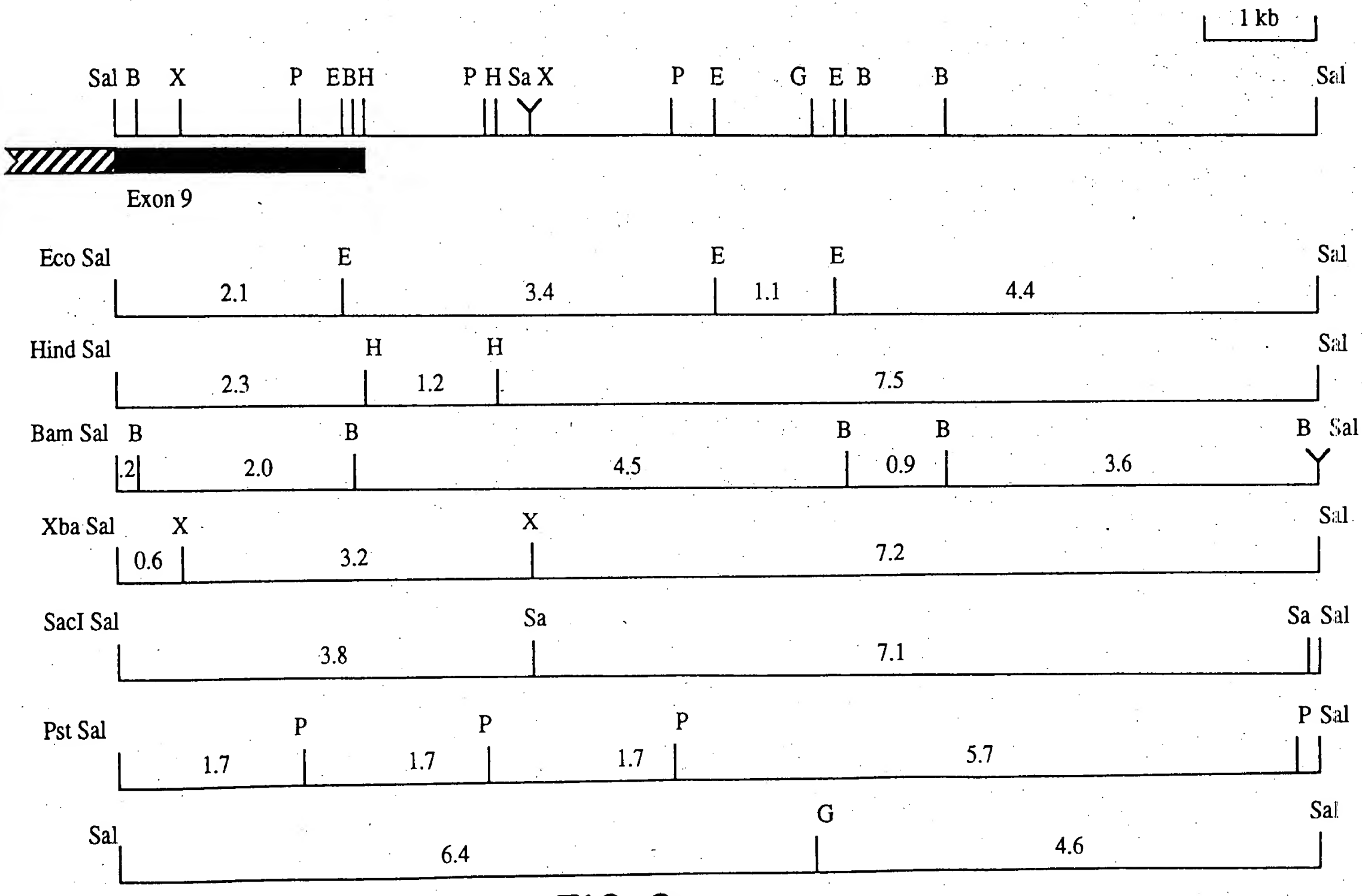


FIG. 9a

No sites for: Xho,Kpn, SacII, Sma, Cla, EcoRV, Apa, Not, PvuI, Nde

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn ....

A	ApaI
B	BamHI
C	ClaI
E	EcoRI
G	BglII
H	HindIII
K	KpnI
N	NotI
P	PstI
S	Sal
Sa	SacI
V	EcoRV
X	XbaI
Xh	XhoI

FIG. 9b

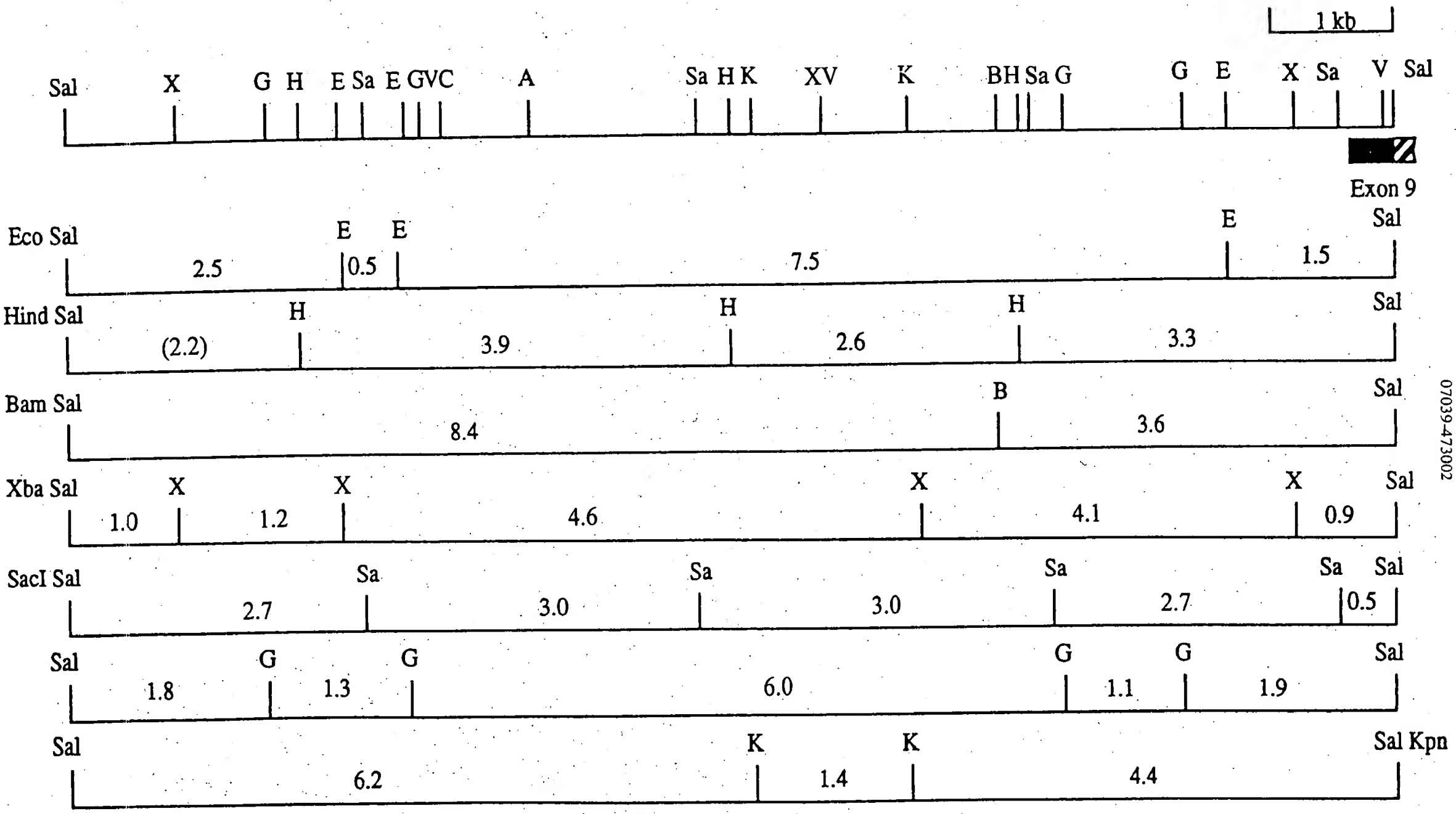
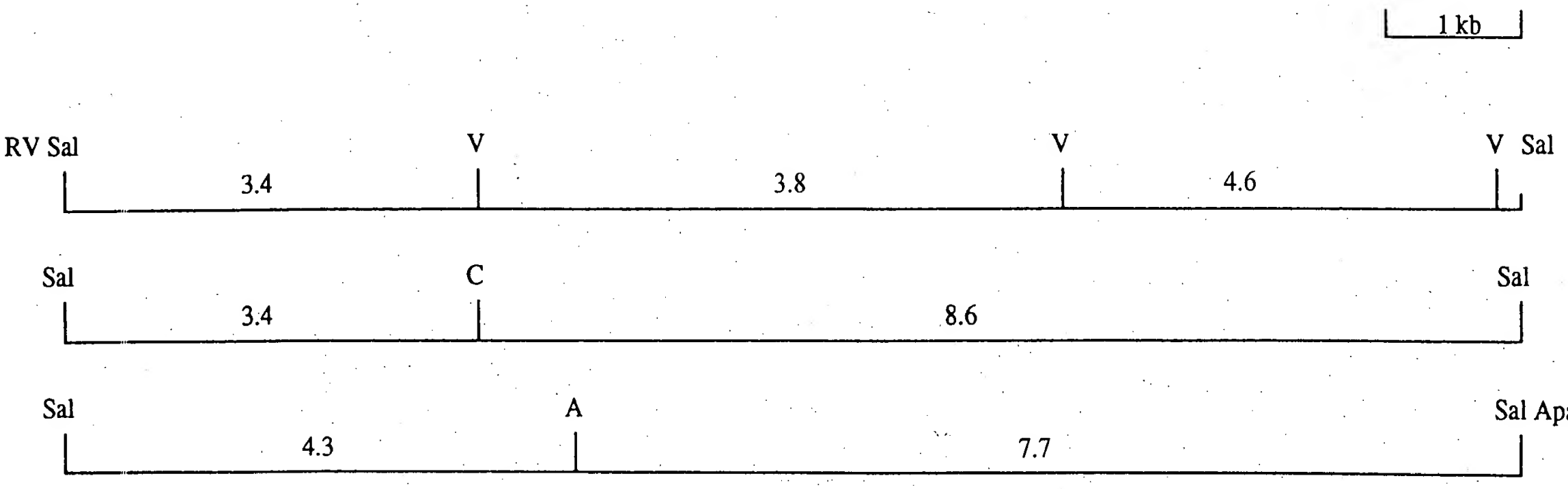


FIG. 10a



No sites for: Xho, SacII, Sma, Not

A ApaI
B BamHI
C ClaI
E EcoRI
G BglII
H HindIII
K KpnI
N NotI
P PstI
S Sal
Sa SacI
V EcoRV
X XbaI
Xh XhoI

pUBS:

----SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn----

FIG. 10b

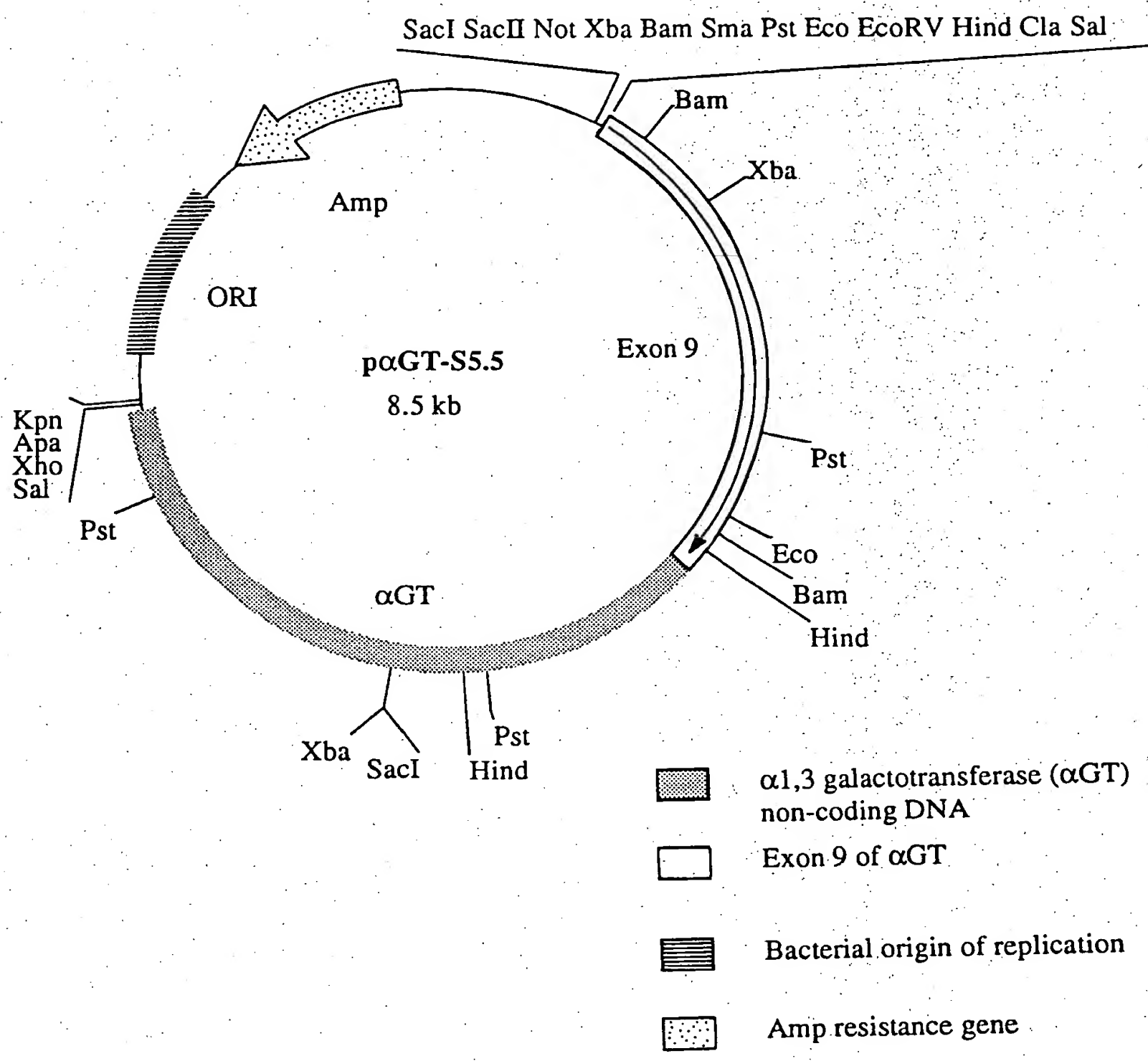


FIG. 11

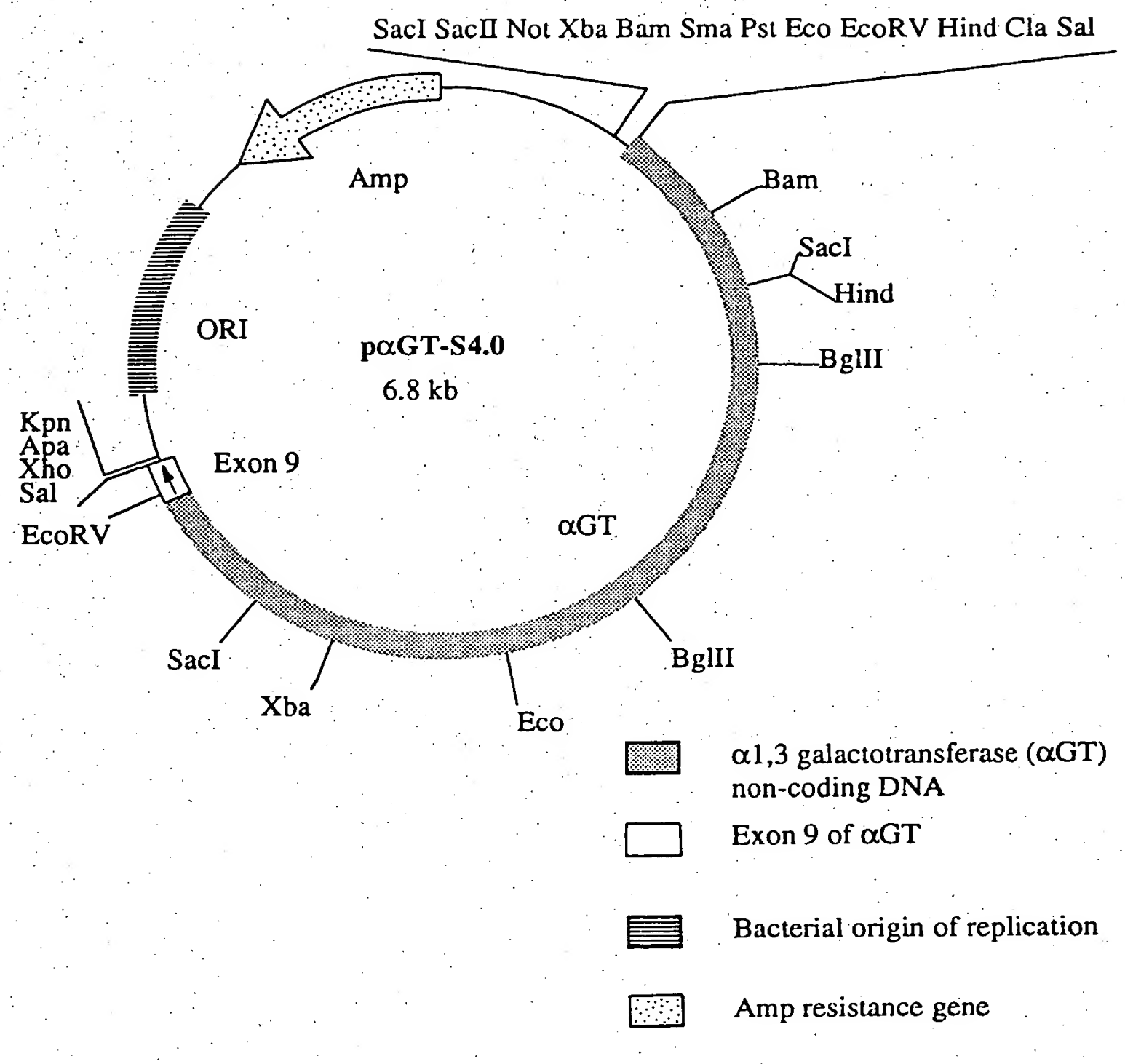
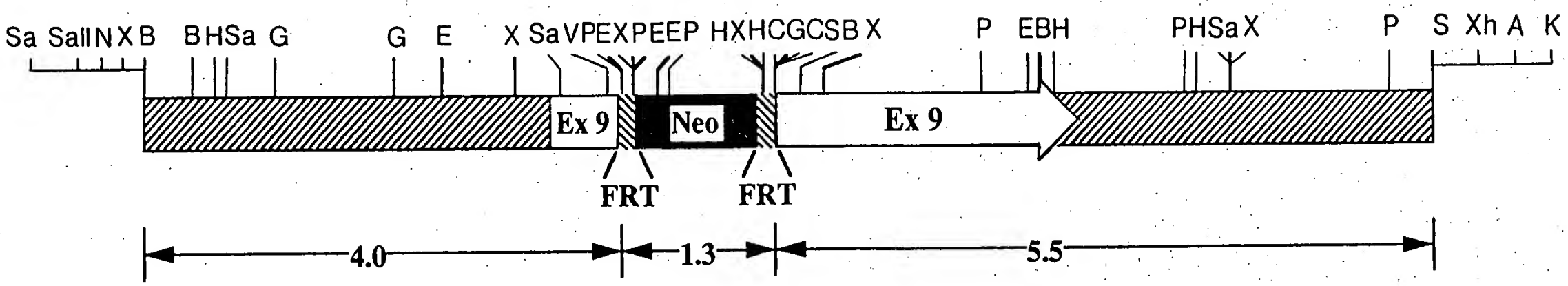


FIG. 12



Region around Cla-Bgl linker

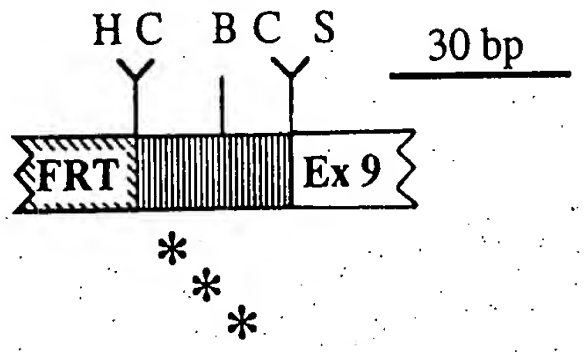


FIG. 13

A ApaI
B BamHI
C ClaI
E EcoRI
G BglII
H HindIII
K KpnI
N NotI
P PstI
S SalI
Sa SacI
V EcoRV
X XbaI
Xh XhoI

α1,3 galactotransferase (αGT) non-coding DNA

Exon 9 of αGT

Neo resistance gene

FRT recombination site

Cla-Bgl-Cla linker

* Stop codons

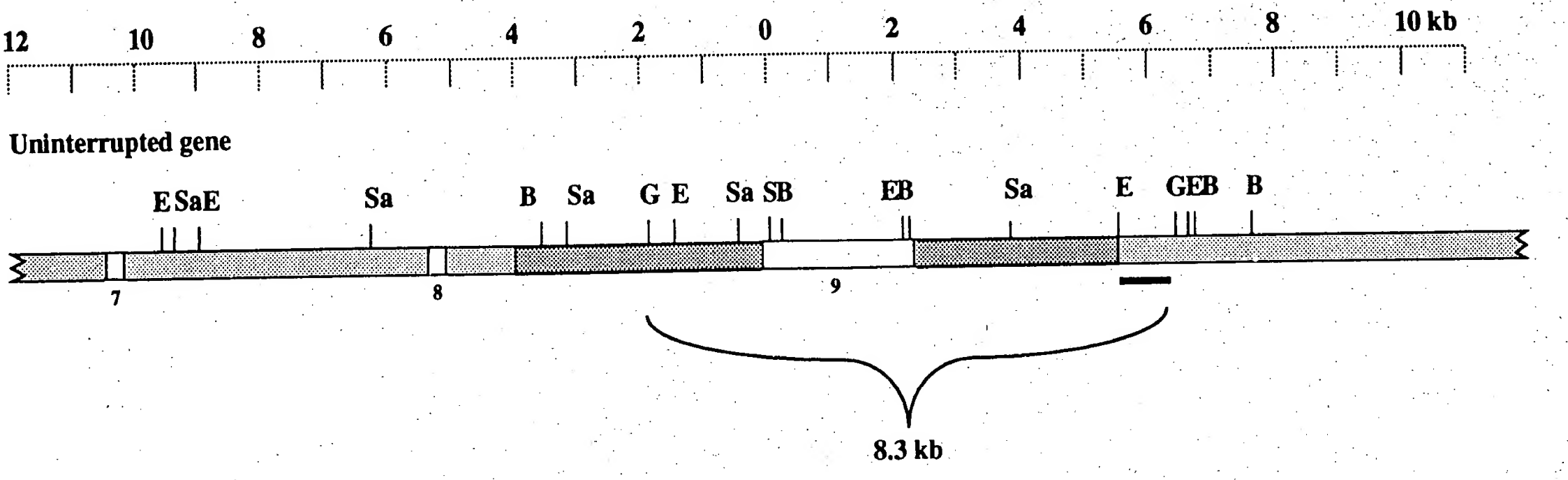


FIG. 14

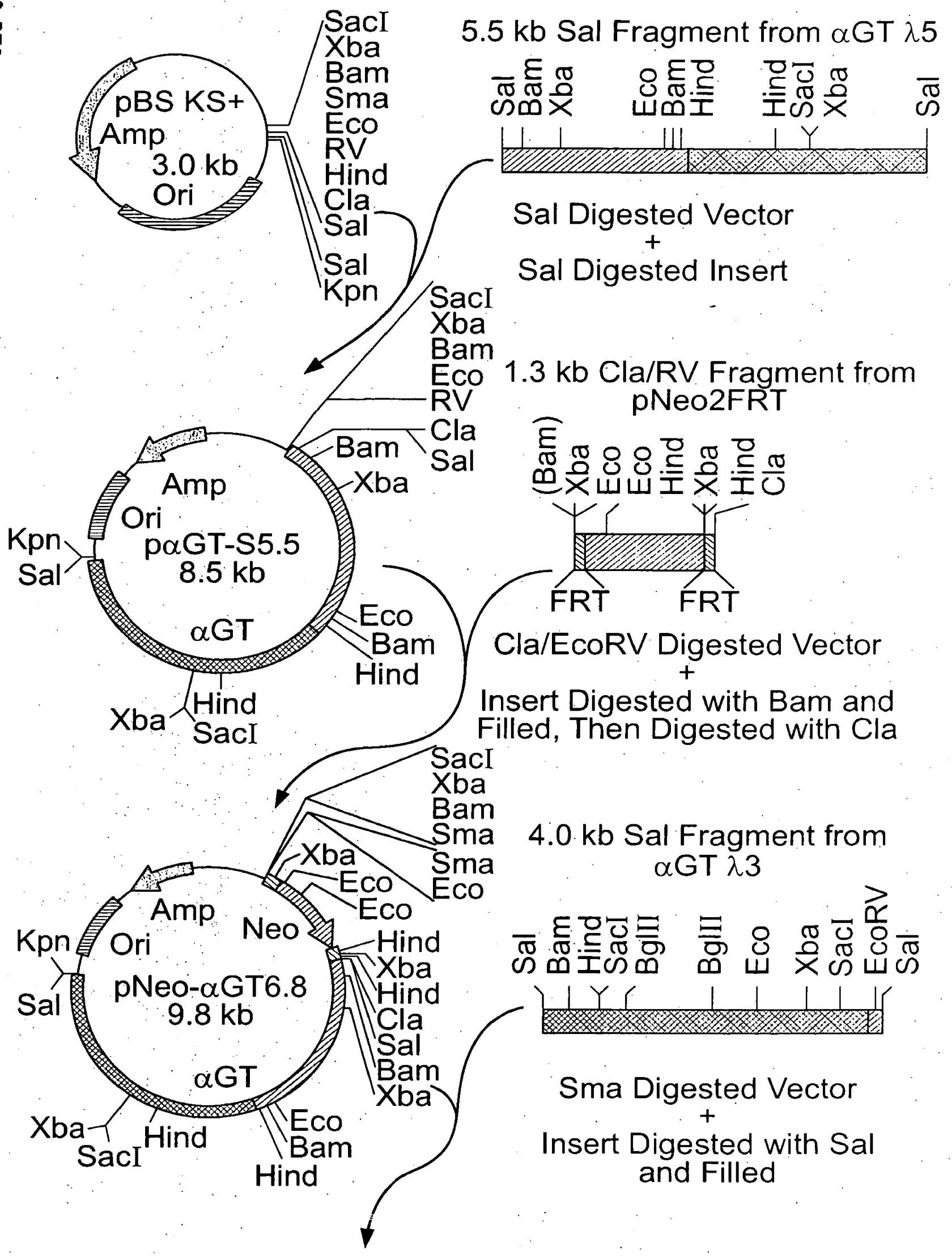


FIG. 15A

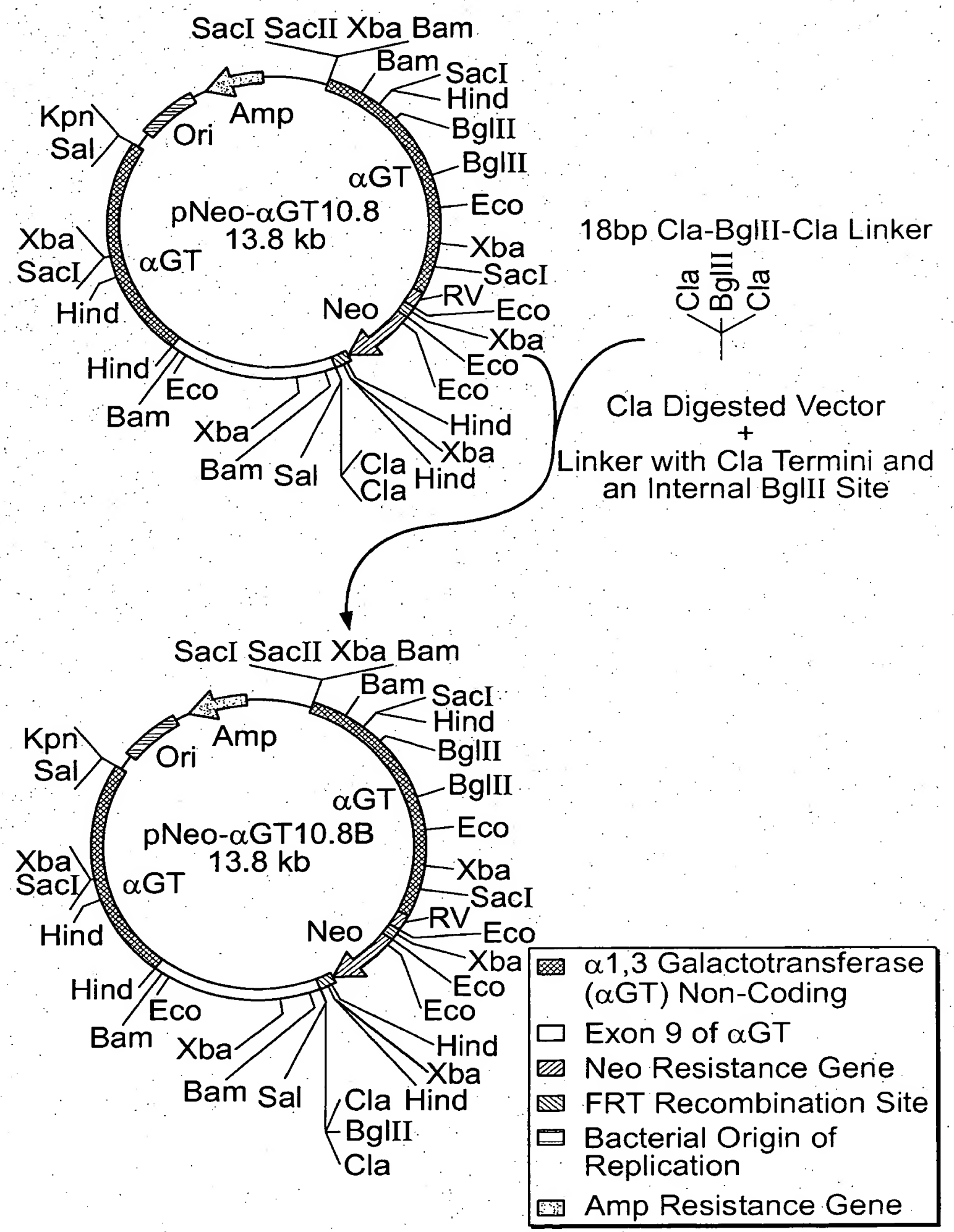


FIG. 15B

```
        10          20          30          40          50          60
GAGGGCTGCA GGAATTCGAT GATCCCCCAG CTTGAAGTTC CTATTCCGAA GTTCCTATTC

        70          80          90         100         110         120
TCTAGAAAGT ATAGGAACTT CAAGCTGGGC TGCAGGAATT CGATTCGAGC AGTGTGGTTT

       130         140         150         160         170         180
TGCAAGAGGA AGCAAAAAGC CTCTCCACCC AGGCCTGGAA TGTTTCCACC CAATGTCGAG

       190         200         210         220         230         240
CAGTGTGGTT TTGCAAGAGG AAGCAAAAAG CCTCTCCACC CAGGCCTGGA ATGTTTCCAC

       250         260         270         280         290         300
CCAATGTCGA GCAAACCCCG CCCAGCGTCT TGTCATTGGC GAATTCGAAC ACGCAGATGC

       310         320         330         340         350         360
AGTCGGGGCG GCGCGGTCCC AGGTCCACTT GGCATATTAA GGTGACGCGT GTGGCCTCGA

       370         380         390         400         410         420
ACACCGAGCG ACCCTGCAGC CAATATGGGA TCGGCCATTG AACAAGATGG ATTGCACGCA

       430         440         450         460         470         480
GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA TTCGGCTATG ACTGGGCACA ACAGACAATC

       490         500         510         520         530         540
GGCTGCTCTG ATGCCGCCGT GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTTGTC

       550         560         570         580         590         600
AAGACCGACC TGTCCGGTGC CCTGAATGAA CTCCAAGACG AGGCAGCGCG GCTATCGTGG

       610         620         630         640         650         660
CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG TTGTCACTGA AGCGGGAAGG

       670         680         690         700         710         720
GACTGGCTGC TATTGGGCGA AGTGCCGGGG CAGGATCTCC TGTCATCTCA CCTTGCTCCT

       730         740         750         760         770         780
GCCGAGAAAG TATCCATCAT GGCTGATGCA ATGCGGCGGC TGCATACGCT TGATCCGGCT

       790         800         810         820         830         840
ACCTGCCCAT TCGACCACCA AGCGAAACAT CGCATCGAGC GAGCACGTAC TCGGATGGAA

       850         860         870         880         890         900
GCCGGTCTTG TCGATCAGGA TGATCTGGAC GAAGAGCATC AGGGGCTCGC GCCAGCCGAA

       910         920         930         940         950         960
CTGTTCGCCA GGCTCAAGGC GCGGATGCCC GACGGCGAGG ATCTCGTCGT GACCCATGGC

       970         980         990        1000        1010        1020
GATGCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT TTTCTGGATT CATCGACTGT

      1030        1040        1050        1060        1070        1080
GGCCGGCTGG GTGTGGCGGA CCGCTATCAG GACATAGCGT TGGCTACCCG TGATATTGCT

      1090        1100        1110        1120        1130        1140
GAAGAGCTTG GCGGCGAATG GGCTGACCGC TTCCTCGTGC TTTACGGTAT CGCCGCTCCC
```

FIG. 16A

```
      1150        1160        1170        1180        1190        1200
GATTCGCAGC GCATCGCCTT CTATCGCCTT CTTGACGAGT TCTTCTGAGG GGATCGGCAA

      1210        1220        1230        1240        1250        1260
TAAAAAGACA GAATAAAACG CACGGGTGTT GGGCGTTTGT TCGGATCATC AAGCTTGAAG

      1270        1280        1290        1300        1310        1320
TTCCTATTCC GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTCAAGCTT ATCGATGAGT

      1330        1340        1350        1360        1370        1380
AGATCTTGAT CGATACCGTC ..........  ..........  ..........  ..........
```

Linker sequences : 0-28

FRT : 29-104

Polyoma virus enhancer repeats : 105-249

Herpes Simplex Virus Tyrosine Kinase promoter : 250-385

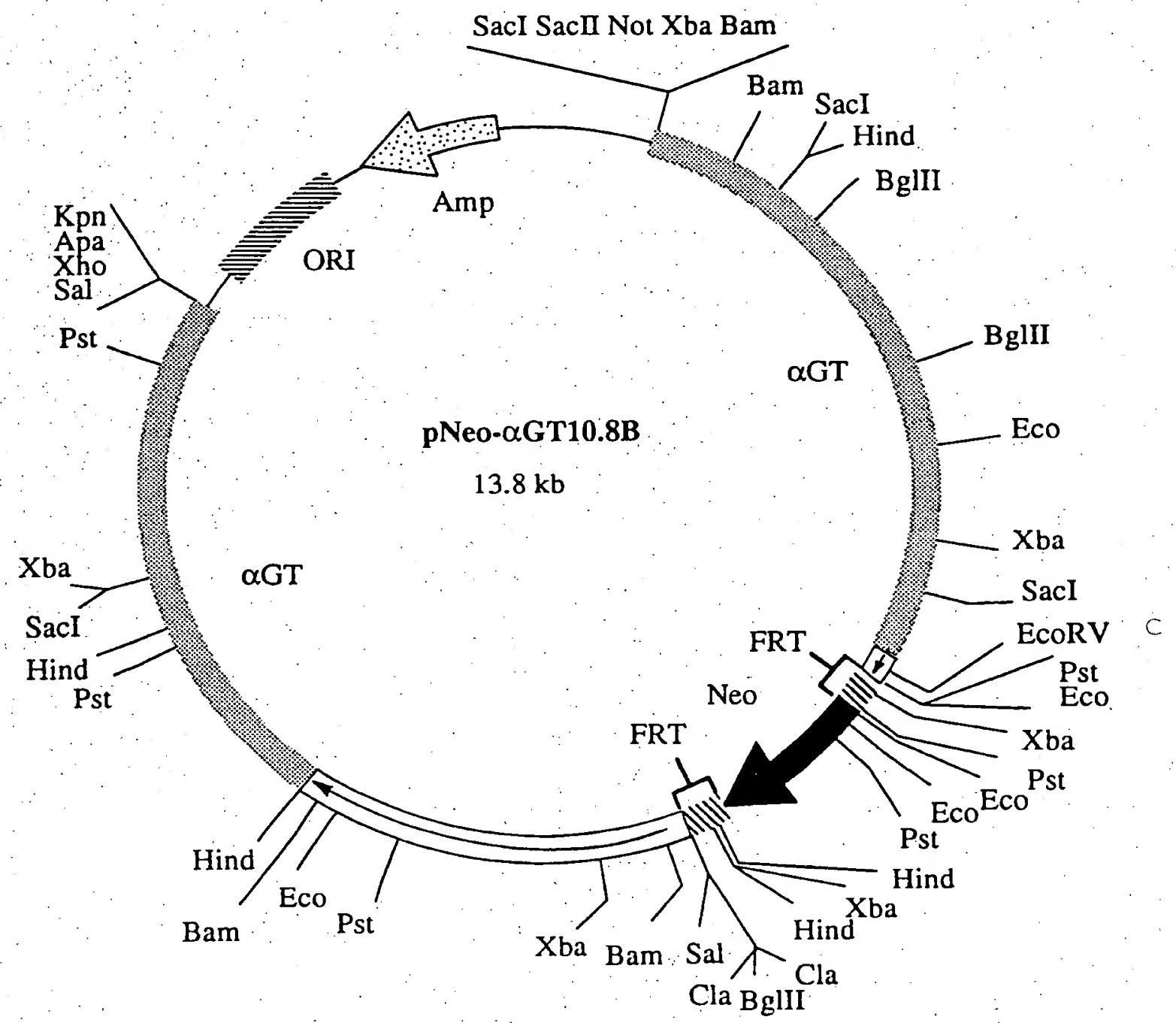
Neomycin phosphotransferase coding region : 385-1188

Herpes Simplex Virus Tyrosine Kinase PolyA signal : 1189-1249

FRT : 1250-1310

Linker sequences : 1311-1340

FIG. 16B



α1,3 galactotransferase (αGT) non-coding DNA

Exon 9 of αGT

Neo resistance gene

FRT recombination site

Bacterial origin of replication

Amp resistance gene

FIG. 17

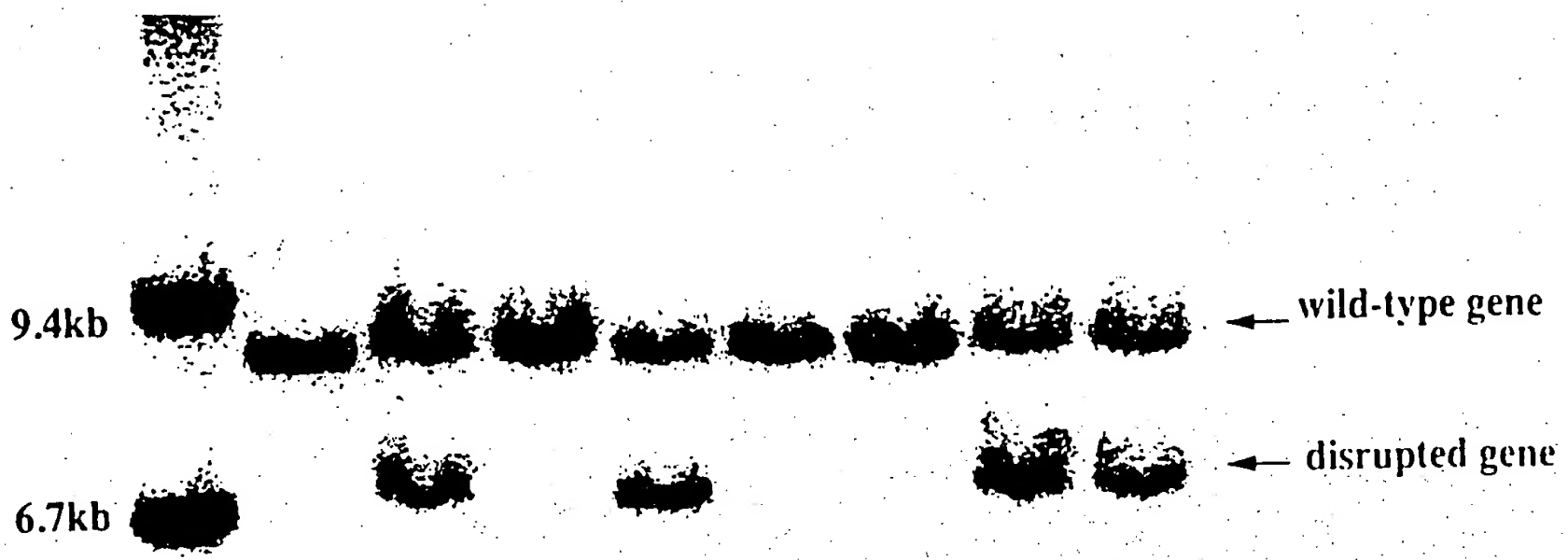


FIG. 18

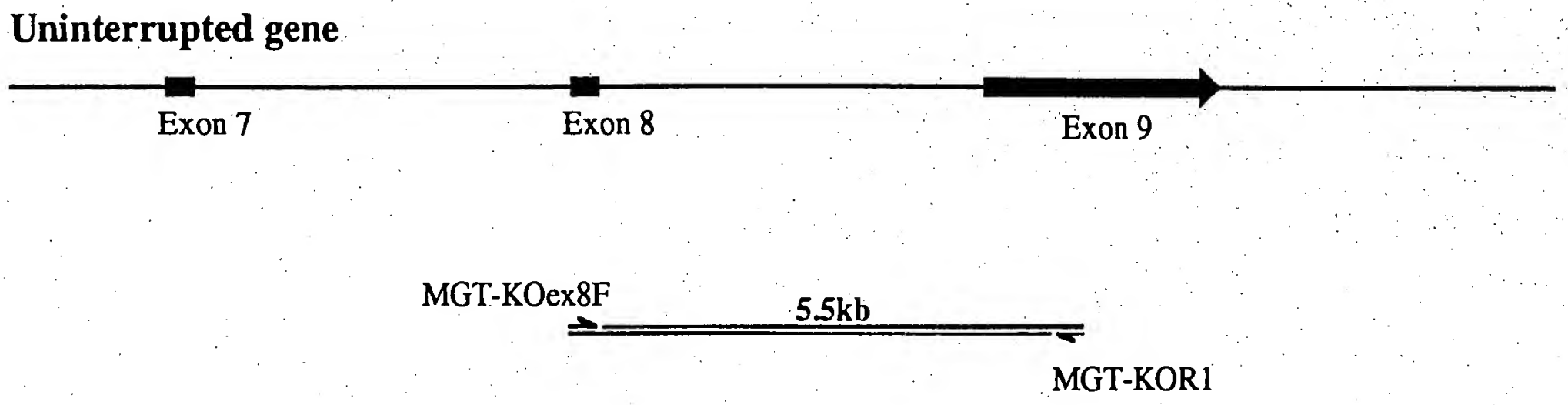
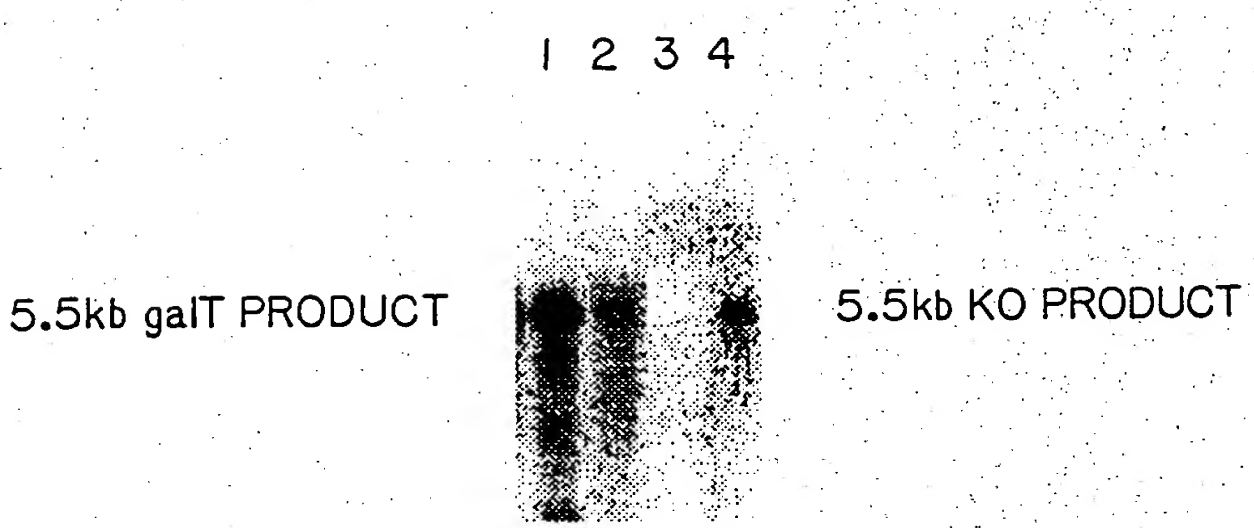


FIG. 19

MATERIALS AND METHODS FOR MANAGEMENT OF HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
Anthony J.F. D'Apice et al.
08/984,900
07039-473002



1. CBAC TEMPLATE; WILD TYPE PRIMERS
2. 7C2 TEMPLATE; WILD TYPE PRIMERS
3. CBAC TEMPLATE; KO PRIMERS
4. 7C2 TEMPLATE; KO PRIMERS

FIG. 20

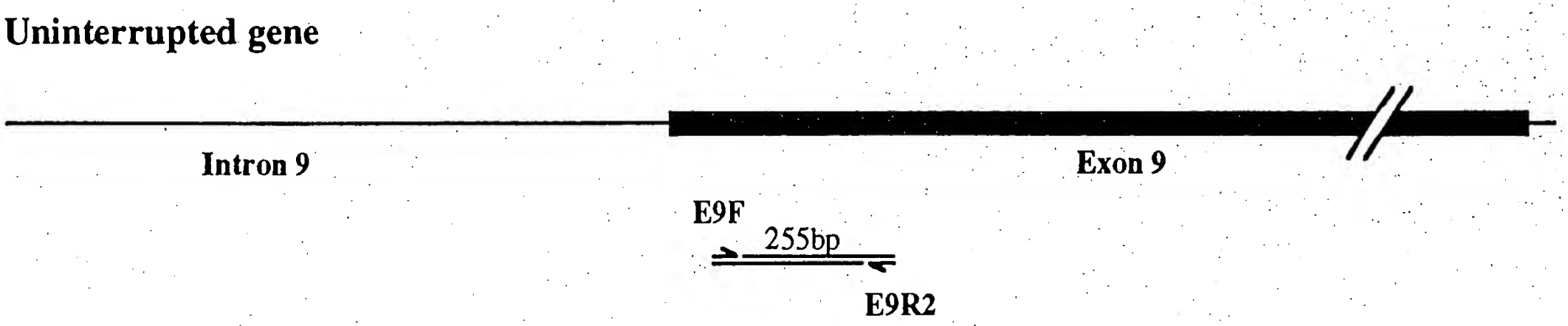


FIG. 21

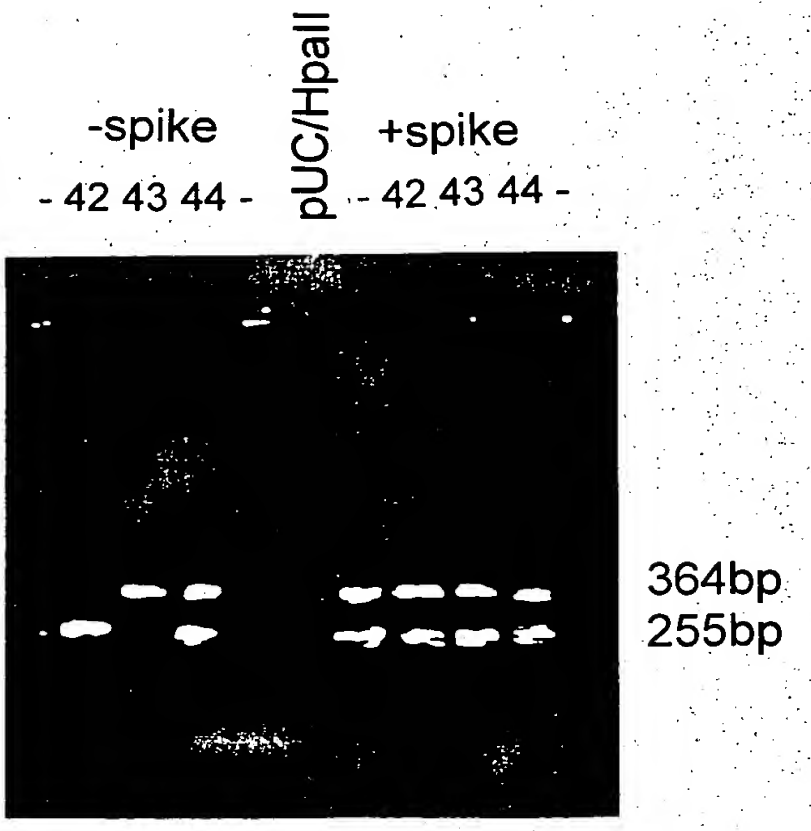
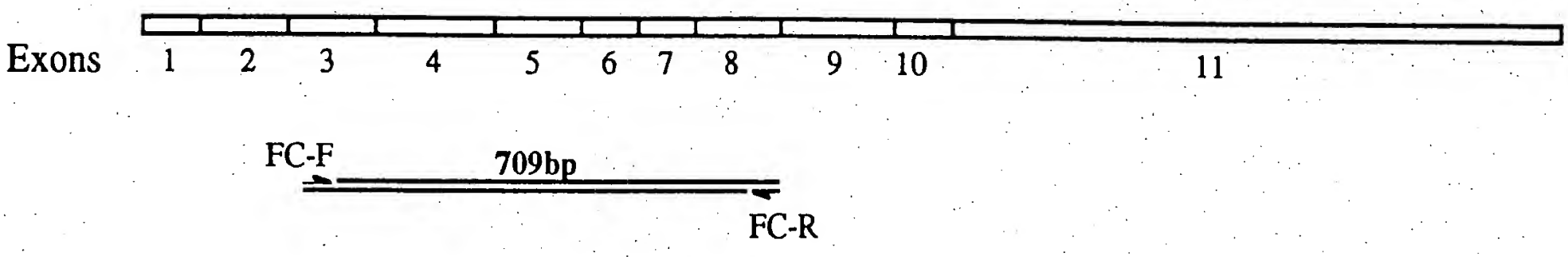


FIG. 22

Primer binding sites within mouse ferrochelatase cDNA



Primer binding sites within mouse α-1,3-GalT cDNA

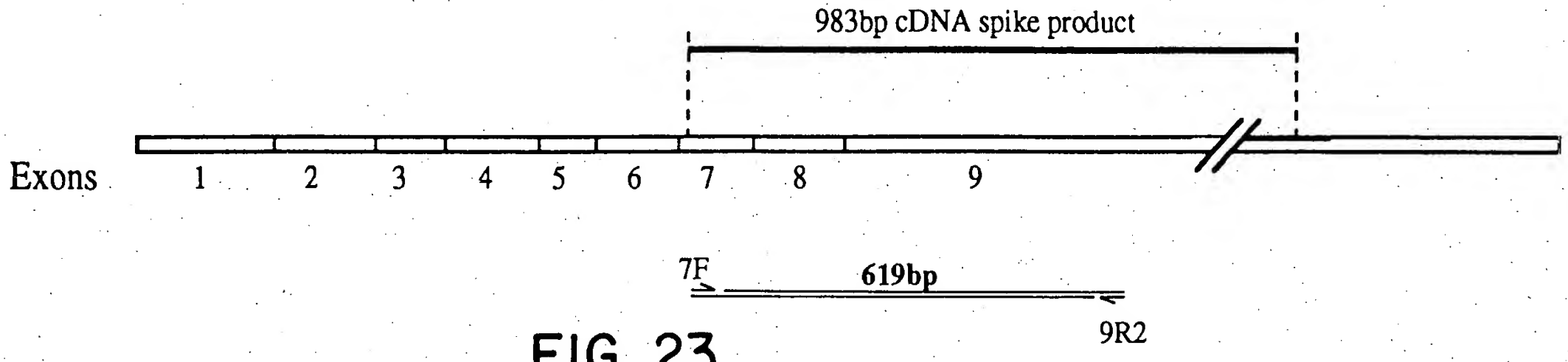
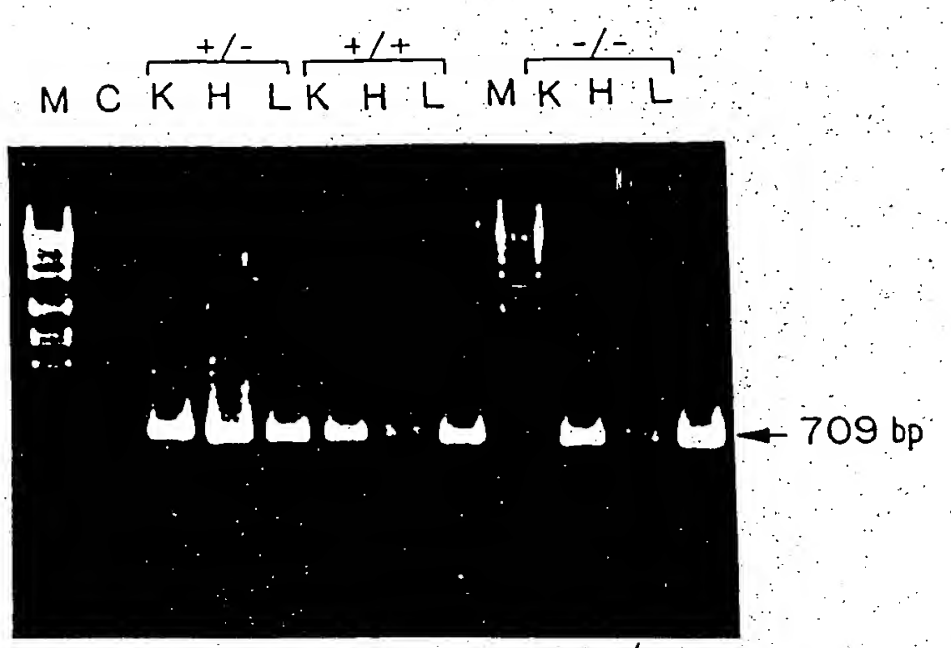


FIG. 23

i) Ferrochelatase, FC-F/R

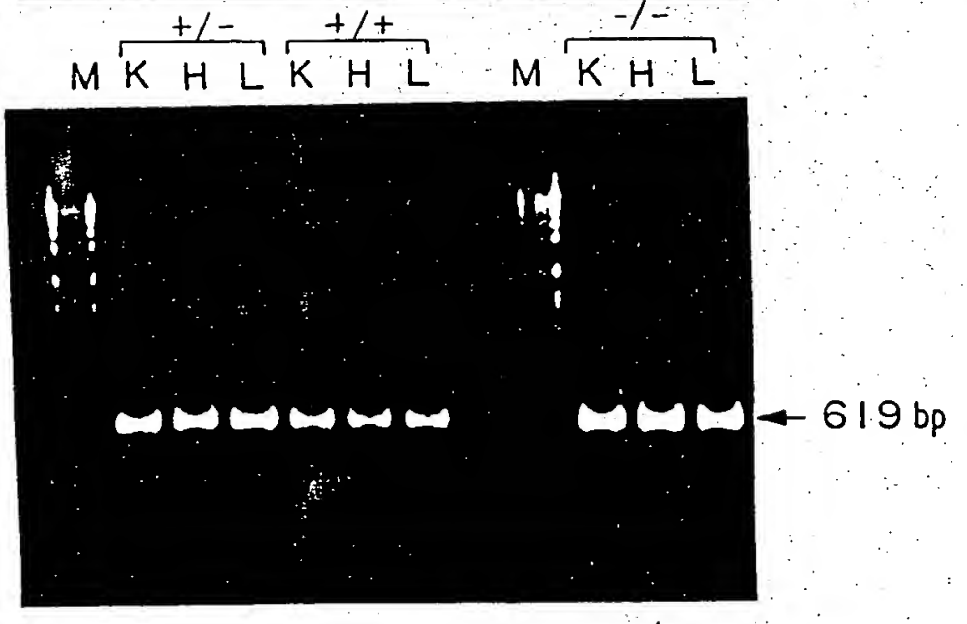
M, Marker SPP-I
C, MQW control
K, KIDNEY
H, HEART
L, LIVER

FIG. 24a



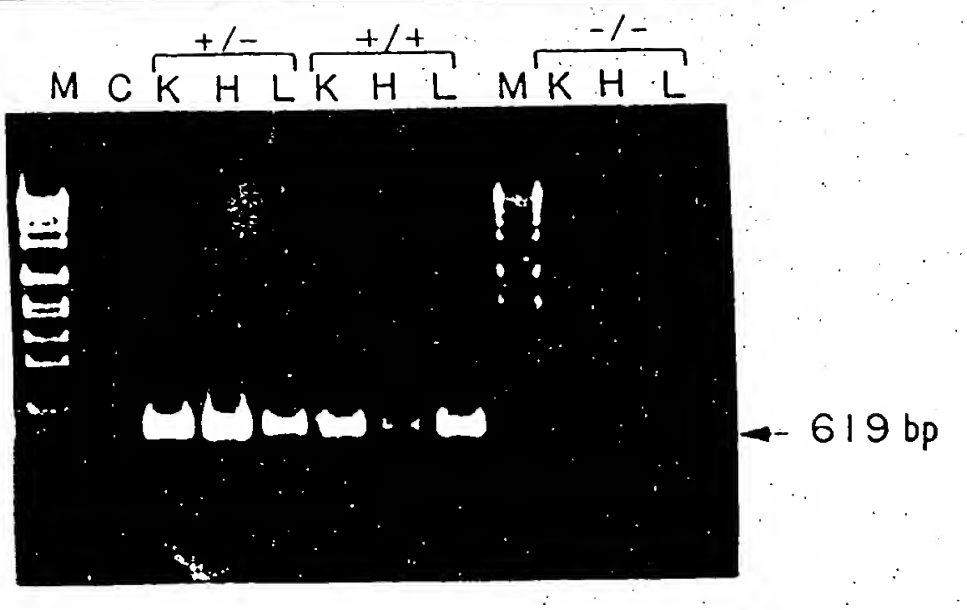
ii) α-1,3-GT cDNA spike
+ 7F/9R2 primers

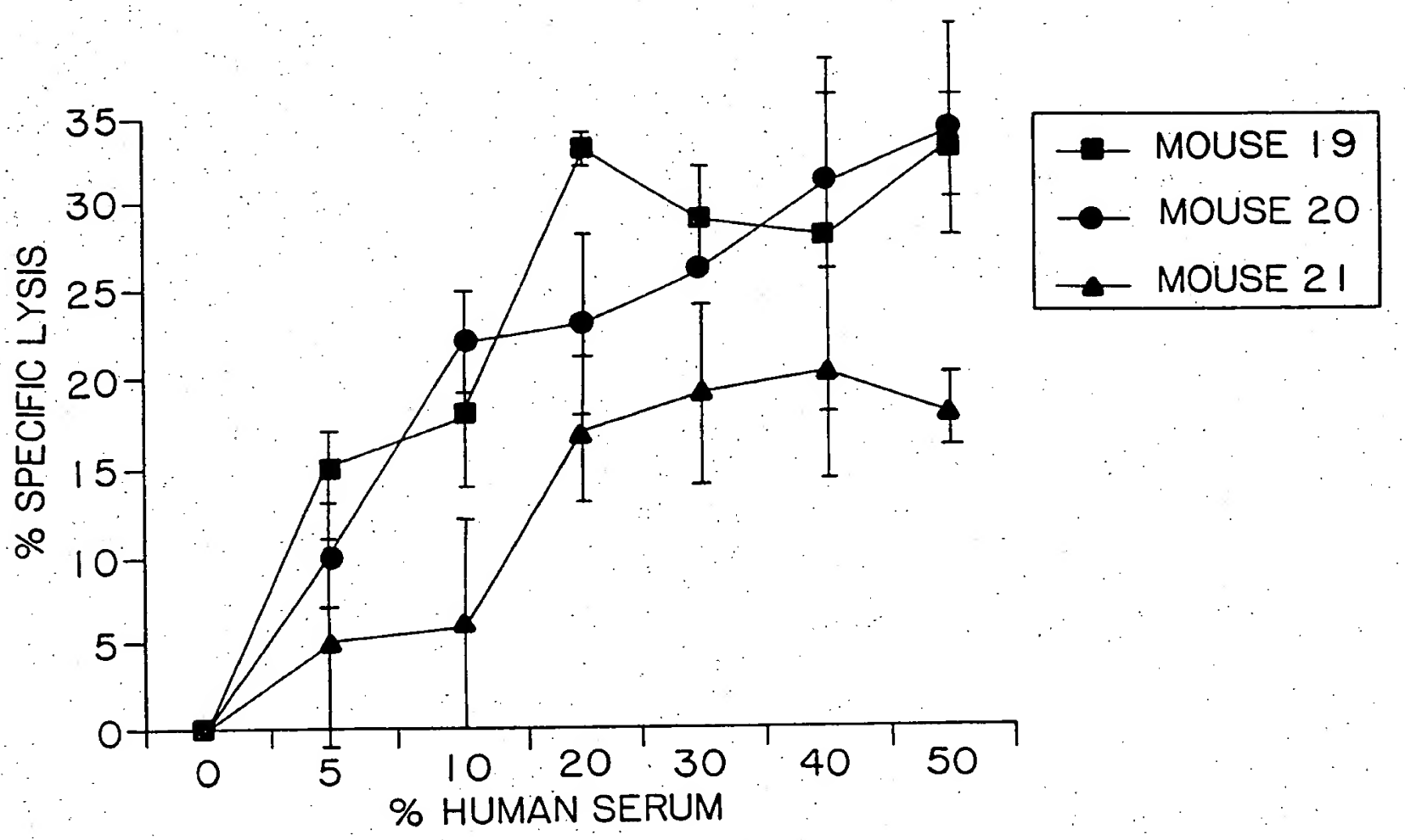
FIG. 24b



iii) α-1,3-GT
7F/9R2 primers

FIG. 24c





MOUSE 19: WILD TYPE; MOUSE 20: HETEROZYGOTC Gal KO; MOUSE 21: HOMOZYGOUS Gal KO

FIG. 25

T-LIF SEQUENCE - Murine

CTGACACCTTTCGCTTTCCTCTTGCGTGTCCGCCTGCGACCTTTCCCCACCCC

GGCCTCTTTCCTGGTTGCACCACTTCCTCTCATTCCAAAGGATTGTGCCCTTA

CTGCTGCTGGTTCTGCACTGGAAACACGGGGCAGGGAGCCCTCTTCCCATCAC

CCCTGTAAATGCCACCTGTGCCATACGCCACCCATGCCACGGCAACCTC

Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly
ATG AAC CAG ATC AAG AAT CAA CTG GCA CAG CTC AAT GGC

Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly
AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA GCT CAA GGX

Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro Asn
GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT AAC

Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys
ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG

Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser
ACC AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC

Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
GCC TCC CTG ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC

Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile
CCC ACT GCC GTG AGC CTC CAG GTC AAG CTC AAT GCT ACT ATA

Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu
GAC GTC ATG AGG GGC CTC CTC AGC AAT GTG CTT TGC CGT CTG

Cys Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val
TGC AAC AAG TAC CGT GTG GGC CAC GTG GAT GTG CCA CCT GTC

Pro Asp His Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu
CCC GAC CAC TCT GAC AAA GAA GCC TTC CAA AGG AAA AAG TTG

Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser Val
GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT GTG

Val Val Gln Ala Phe ***
GTG GTC CAG GCC TTC TAG AGAGGAGGTCTTGAATGTACCATGGACTG...

FIG. 26

HUMAN T-LIF SEQUENCE

```
GACCTTTTGC CTTTTCTCTC TCCTGGTGCA CCATTTCCTC TCCCTCCCTG      50
AGCCGGAGTT GTGCCCCTGC TGTTGGTTCT GCACTGGAAA CATGGGGCGG     100
GGAGCCCCCT CCCCATCACC CCTGTCAACG CCACCTGTGC CATACGCCAC     150
CCATGTCACA ACAACCTC ATG AAC CAG ATC                        182
                    Met Asn Gln Ile
AGG AGC CAA CTG GCA CAG CTC AAT GGC AGT GCC AAT GCC CTC     227
Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu
5                   10                  15
TTT ATT CTC TAT TAC ACA GCC CAG GGG GAG CCG TTC CCC AAC     272
Phe Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn
    20                  25                  30
AAC CTG GAC AAG CTA TGT GGC CCC AAC GTG ACG GAC TTC CCG     317
Asn Leu Asp Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro
        35                  40                  45
CCC TTC CAC GCC AAC GGC ACG GAG AAG GCC AAG CTG GTG GAG     362
Pro Phe His Ala Asn Gly Thr Glu Lys Ala Lys Leu Val Glu
            50                  55                  60
CTG TAC CGC ATA GTC GTG TAC CTT GGC ACC TCC CTG GGC AAC     407
Leu Tyr Arg Ile Val Val Tyr Leu Gly Thr Ser Leu Gly Asn
                65                  70
ATC ACC CGG GAC CAG AAG ATC CTC AAC CCC AGT GCC CTC AGC     452
Ile Thr Arg Asp Gln Lys Ile Leu Asn Pro Ser Ala Leu Ser
75                  80                  85
CTC CAC AGC AAG CTC AAC GCC ACC GCC GAC ATC CTG CGA GGC     497
Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile Leu Arg Gly
    90                  95                  100
CTC CTT AGC AAC GTG CTG TGC CGC CTG TGC AGC AAG TAC CAC     542
Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr His
        105                 110                 115
GTG GGC CAT GTG GAC GTG ACC TAC GGC CCT GAC ACC TCG GGT     587
Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly
            120                 125                 130
AAG GAT GTC TTC CAG AAG AAG AAG CTG GGC TGT CAA CTC CTG     632
Lys Asp Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu
                135                 140
GGG AAG TAT AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC     677
Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe
145                 150                 155
TAG CAGGAGGTCT                                             722
***
```

FIG. 27

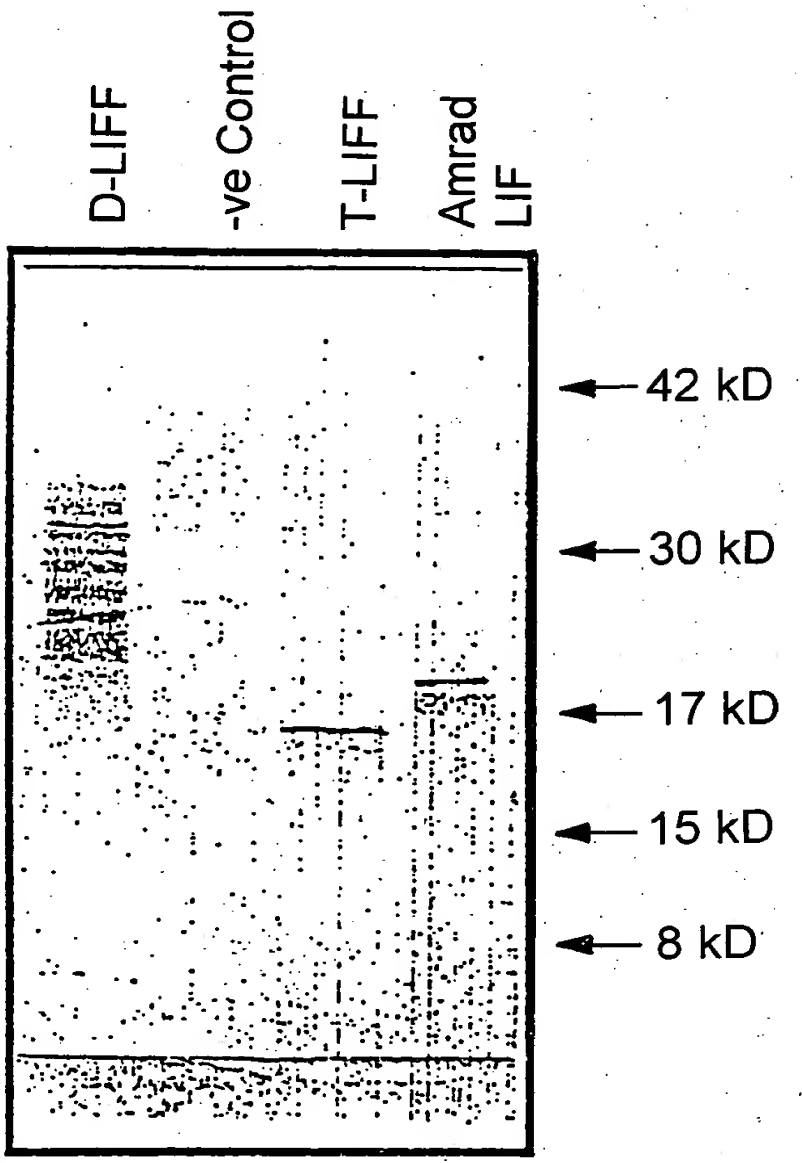


FIG. 28

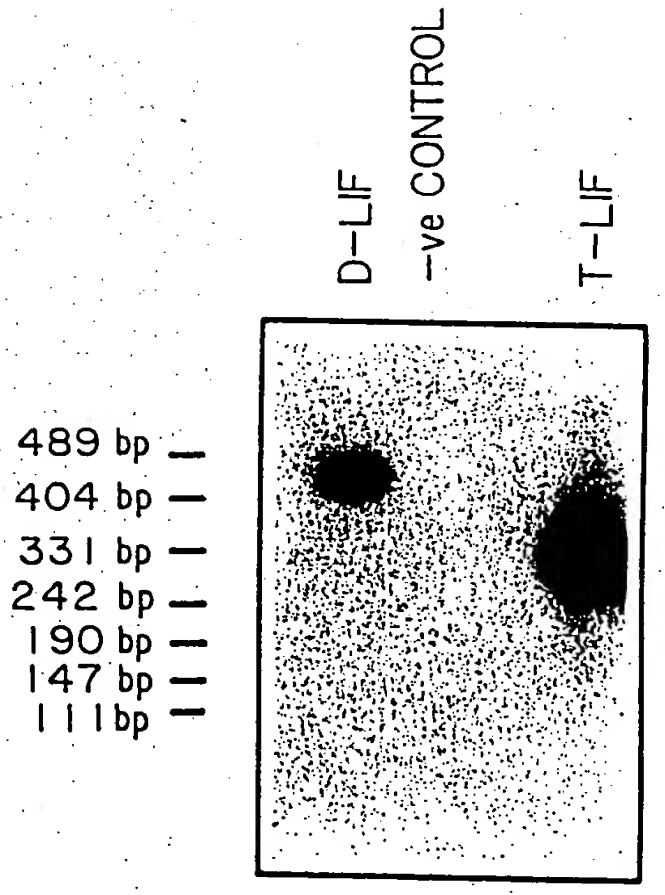
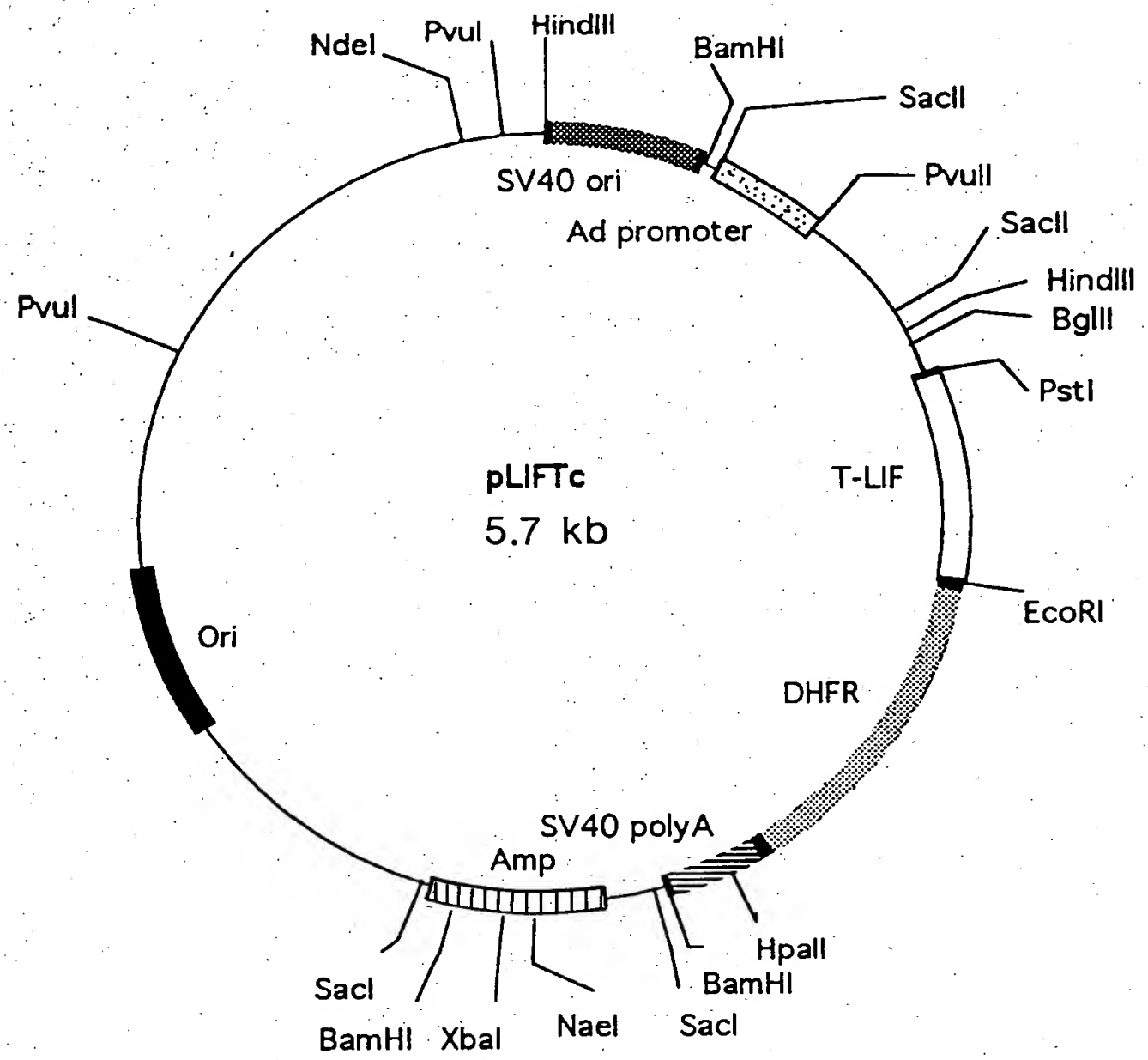


FIG. 30



Dihydrofolate reductase 3' end

Adenovirus promoter

SV40 origin of replication

T-LIF coding region

Bacterial origin of replication

Ampicillin resistance gene

FIG. 29